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(54) Title: IMPROVED ADENOVIRUS AND METHODS OF USE THEREOF			
(57) Abstract <p>A recombinant adenovirus and a method for producing the virus are provided which utilize a recombinant shuttle vector comprising adenovirus DNA sequence for the 5' and 3' cis-elements necessary for replication and virion encapsidation in the absence of sequence encoding viral genes and a selected minigene linked thereto, and a helper adenovirus comprising sufficient adenovirus gene sequences necessary for a productive viral infection. Desirably the helper gene is crippled by modifications to its 5' packaging sequences, which facilitates purification of the viral particle from the helper virus.</p>			

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IMPROVED ADENOVIRUS AND METHODS OF USE THEREOF

This invention was supported by the National
Institute of Health Grant No. P30 DK 47757. The United
5 States government has rights in this invention.

Field of the Invention

The present invention relates to the field of
vectors useful in somatic gene therapy and the production
10 thereof.

Background of the Invention

Human gene therapy is an approach to treating human
disease that is based on the modification of gene
15 expression in cells of the patient. It has become
apparent over the last decade that the single most
outstanding barrier to the success of gene therapy as a
strategy for treating inherited diseases, cancer, and
other genetic dysfunctions is the development of useful
20 gene transfer vehicles. Eukaryotic viruses have been
employed as vehicles for somatic gene therapy. Among the
viral vectors that have been cited frequently in gene
therapy research are adenoviruses.

Adenoviruses are eukaryotic DNA viruses that can be
25 modified to efficiently deliver a therapeutic or reporter
transgene to a variety of cell types. Recombinant
adenoviruses types 2 and 5 (Ad2 and Ad5, respectively),
which cause respiratory disease in humans, are currently
being developed for gene therapy. Both Ad2 and Ad5
30 belong to a subclass of adenovirus that are not
associated with human malignancies. Recombinant
adenoviruses are capable of providing extremely high
levels of transgene delivery to virtually all cell types,
regardless of the mitotic state. High titers (10^{13}
35 plaque forming units/ml) of recombinant virus can be
easily generated in 293 cells (the adenovirus equivalent

to retrovirus packaging cell lines) and cryo-stored for extended periods without appreciable losses. The efficacy of this system in delivering a therapeutic transgene *in vivo* that complements a genetic imbalance has been demonstrated in animal models of various disorders [Y. Watanabe, Atherosclerosis, 36:261-268 (1986); K. Tanzawa et al, FEBS Letters, 118(1):81-84 (1980); J.L. Golasten et al, New Engl. J. Med., 309(11983):288-296 (1983); S. Ishibashi et al, J. Clin. Invest., 92:883-893 (1993); and S. Ishibashi et al, J. Clin. Invest., 93:1885-1893 (1994)]. Indeed, a recombinant replication defective adenovirus encoding a cDNA for the cystic fibrosis transmembrane regulator (CFTR) has been approved for use in at least two human CF clinical trials [see, e.g., J. Wilson, Nature, 365:691-692 (Oct. 21, 1993)]. Further support of the safety of recombinant adenoviruses for gene therapy is the extensive experience of live adenovirus vaccines in human populations.

Human adenoviruses are comprised of a linear, approximately 36 kb double-stranded DNA genome, which is divided into 100 map units (m.u.), each of which is 360 bp in length. The DNA contains short inverted terminal repeats (ITR) at each end of the genome that are required for viral DNA replication. The gene products are organized into early (E1 through E4) and late (L1 through L5) regions, based on expression before or after the initiation of viral DNA synthesis [see, e.g., Horwitz, Virology, 2d edit., ed. B. N. Fields, Raven Press, Ltd., New York (1990)].

The first-generation recombinant, replication-deficient adenoviruses which have been developed for gene therapy contain deletions of the entire E1a and part of the E1b regions. This replication-defective virus is grown on an adenovirus-transformed, complementation human

embryonic kidney cell line containing a functional adenovirus E1a gene which provides a transacting E1a protein, the 293 cell [ATCC CRL1573]. E1-deleted viruses are capable of replicating and producing infectious virus in the 293 cells, which provide E1a and E1b region gene products in trans. The resulting virus is capable of infecting many cell types and can express the introduced gene (providing it carries its own promoter), but cannot replicate in a cell that does not carry the E1 region DNA unless the cell is infected at a very high multiplicity of infection.

However, *in vivo* studies revealed transgene expression in these E1 deleted vectors was transient and invariably associated with the development of severe inflammation at the site of vector targeting [S. Ishibashi et al, J. Clin. Invest., 93:1885-1893 (1994); J. M. Wilson et al, Proc. Natl. Acad. Sci., USA, 85:4421-4424 (1988); J. M. Wilson et al, Clin. Bio., 3:21-26 (1991); M. Grossman et al, Som. Cell. and Mol. Gen., 17:601-607 (1991)]. One explanation that has been proposed to explain this finding is that first generation recombinant adenoviruses, despite the deletion of E1 genes, express low levels of other viral proteins. This could be due to basal expression from the unstimulated viral promoters or transactivation by cellular factors. Expression of viral proteins leads to cellular immune responses to the genetically modified cells, resulting in their destruction and replacement with nontransgene containing cells.

There yet remains a need in the art for the development of additional adenovirus vector constructs for gene therapy.

Summary of the Invention

In one aspect, the invention provides the components of a novel recombinant adenovirus production system. One component is a shuttle plasmid, pAdA, that comprises
5 adenovirus cis-elements necessary for replication and virion encapsidation and is deleted of all viral genes. This vector carries a selected transgene under the control of a selected promoter and other conventional vector/plasmid regulatory components. The other
10 component is a helper adenovirus, which alone or with a packaging cell line, supplies sufficient gene sequences necessary for a productive viral infection. In a preferred embodiment, the helper virus has been altered to contain modifications to the native gene sequences
15 which direct efficient packaging, so as to substantially disable or "cripple" the packaging function of the helper virus or its ability to replicate.

In another aspect, the present invention provides a unique recombinant adenovirus, an AdA virus, produced by
20 use of the components above. This recombinant virus comprises an adenovirus capsid, adenovirus cis-elements necessary for replication and virion encapsidation, but is deleted of all viral genes (i.e., all viral open reading frames). This virus particle carries a selected
25 transgene under the control of a selected promoter and other conventional vector regulatory components. This AdA recombinant virus is characterized by high titer transgene delivery to a host cell and the ability to stably integrate the transgene into the host cell
30 chromosome. In one embodiment, the virus carries as its transgene a reporter gene. Another embodiment of the recombinant virus contains a therapeutic transgene.

In another aspect, the invention provides a method for producing the above-described recombinant AdA virus
35 by co-transfecting a cell line (either a packaging cell

line or a non-packaging cell line) with a shuttle vector or plasmid and a helper adenovirus as described above, wherein the transfected cell generates the AdA virus. The AdA virus is subsequently isolated and purified therefrom.

In yet a further aspect, the invention provides a method for delivering a selected gene to a host cell for expression in that cell by administering an effective amount of a recombinant AdA virus containing a therapeutic transgene to a patient to treat or correct a genetically associated disorder or disease.

Other aspects and advantages of the present invention are described further in the following detailed description of the preferred embodiments thereof.

Brief Description of the Figures

Fig. 1A is a schematic representation of the organization of the major functional elements that define the 5' terminus from Ad5 including an inverted terminal repeat (ITR) and a packaging/enhancer domain. The TATA box of the E1 promoter (black box) and E1A transcriptional start site (arrow) are also shown.

Fig. 1B is an expanded schematic of the packaging/enhancer region of Fig. 1A, indicating the five packaging (PAC) domains (A-repeats), I through V. The arrows indicate the location of PCR primers referenced in Figs. 9A and 9B below.

Fig. 2A is a schematic of shuttle vector pAdA.CMVLacZ containing 5' ITR from Ad5, followed by a CMV promoter/enhancer, a LacZ gene, a 3' ITR from Ad5, and remaining plasmid sequence from plasmid pSP72 backbone. Restriction endonuclease enzymes are represented by conventional designations in the plasmid constructs.

Fig. 2B is a schematic of the shuttle vector digested with EcoRI to release the modified AdΔ genome from the pSP72 plasmid backbone.

Fig. 2C is a schematic depiction of the function of the vector system. In the presence of an E1-deleted helper virus Ad.CBhpAP which encodes a reporter minigene for human placenta alkaline phosphatase (hpAP), the AdΔ.CMVLacZ genome is packaged into preformed virion capsids, distinguishable from the helper virions by the presence of the LacZ gene.

Figs. 3A to 3F [SEQ ID NO: 1] report the top DNA strand of the double-stranded plasmid pAdΔ.CMVLacZ. The complementary sequence may be readily obtained by one of skill in the art. The sequence includes the following components: 3' Ad ITR (nucleotides 607-28 of SEQ ID NO: 1); the 5' Ad ITR (nucleotides 5496-5144 of SEQ ID NO: 1); CMV promoter/enhancer (nucleotides 5117-4524 of SEQ ID NO: 1); SD/SA sequence (nucleotides 4507-4376 of SEQ ID NO: 1); LacZ gene (nucleotides 4320-845 of SEQ ID NO: 1); and a poly A sequence (nucleotides 837-639 of SEQ ID NO: 1).

Fig. 4A is a schematic of shuttle vector pAdΔc.CMVLacZ containing an Ad5 5' ITR and 3' ITR positioned head-to-tail, with a CMV enhancer/promoter-LacZ minigene immediately following the 5' ITR, followed by a plasmid pSP72 (Promega) backbone. Restriction endonuclease enzymes are represented by conventional designations in the plasmid constructs.

Fig. 4B is a schematic depiction of the function of the vector system of Fig. 4A. In the presence of helper virus Ad.CBhpAP, the circular pAdΔc.CMVLacZ shuttle vector sequence is packaged into virion heads, distinguishable from the helper virions by the presence of the LacZ gene.

Figs. 5A to 5F [SEQ ID NO: 2] report the top DNA strand of the double-stranded vector pAdΔ.CMVLacZ. The complementary sequence may be readily obtained by one of skill in the art. The sequence includes the following components: 5' Ad ITR (nucleotides 600-958 of SEQ ID NO: 2); CMV promoter/enhancer (nucleotides 969-1563 of SEQ ID NO: 2); SD/SA sequence (nucleotides 1579-1711); LacZ gene (nucleotides 1762-5236 of SEQ ID NO: 2); poly A sequence (nucleotides 5245-5443 of SEQ ID NO: 2); and 3' Ad ITR (nucleotides 16-596 of SEQ ID NO: 2).

Fig. 6 is a schematic of shuttle vector pAdΔ.CBCFTR containing 5' ITR from Ad5, followed by a chimeric CMV enhancer/β actin promoter enhancer, a CFTR gene, a poly-A sequence, a 3' ITR from Ad5, and remaining plasmid sequence from plasmid pSL1180 (Pharmacia) backbone. Restriction endonuclease enzymes are represented by conventional designations in the plasmid constructs.

Figs. 7A to 7H [SEQ ID NO: 3] report the top DNA strand of the double-stranded plasmid pAdΔ.CBCFTR. The complementary sequence may be readily obtained by one of skill in the art. The sequence includes the following components: 5' Ad ITR (nucleotides 9611-9254 of SEQ ID NO: 3); chimeric CMV enhancer/β actin promoter (nucleotides 9241-8684 of SEQ ID NO: 3); CFTR gene (nucleotides 8622-4065 of SEQ ID NO: 3); poly A sequence (nucleotides 3887-3684 of SEQ ID NO: 3); and 3' Ad ITR (nucleotides 3652-3073 of SEQ ID NO: 3). The remaining plasmid backbone is obtained from pSL1180 (Pharmacia).

Fig. 8A illustrates the generation of 5' adenovirus terminal sequence that contained PAC domains I and II by PCR. See, arrows indicating righthand and lefthand (PAC II) PCR products in Fig. 1B.

Fig. 8B illustrates the generation of 5' terminal sequence that contained PAC domains I, II, III and IV by PCR. See, arrows indicating righthand and lefthand (PAC IV) PCR probes in Fig. 1B.

5 Fig. 8C depicts the amplification products subcloned into the multiple cloning site of pAd.Link.1 (IHGT Vector Core) generating pAd.PACII (domains I and II) and pAd.PACIV (domains I, II, III, and IV) resulting in
10 crippled helper viruses, Ad.PACII and Ad.PACIV with modified packaging (PAC) signals.

Fig. 9A is a schematic representation of the subcloning of a human placenta alkaline phosphatase reporter minigene containing the immediate early CMV enhancer/ promoter (CMV), human placenta alkaline
15 phosphatase cDNA (hpAP), and SV40 polyadenylation signal (pA) into pAd.PACII to result in crippled helper virus vector pAd.PACII.CMVhpAP. Restriction endonuclease enzymes are represented by conventional designations in the plasmid constructs.

20 Fig. 9B is a schematic representation of the subcloning of the same minigene of Fig. 9A into pAd.PACIV to result in crippled helper virus vector pAd.PACIV.CMV.hpAP.

Fig. 10 is a flow diagram summarizing the synthesis
25 of an adenovirus-based polycation helper virus conjugate and its combination with a pAdA shuttle vector to result in a novel viral particle complex. CsCl band purified helper adenovirus was reacted with the heterobifunctional crosslinker sulfo-SMCC and the capsid protein fiber is
30 labeled with the nucleophilic maleimide moiety. Free sulfhydryls were introduced onto poly-L-lysine using 2-iminothiolane-HCl and mixed with the labelled adenovirus, resulting in the helper virus conjugate Ad-pLys. A unique adenovirus-based particle is generated by
35 purifying the Ad-pLys conjugate over a CsCl gradient to

remove unincorporated poly-L-lysine, followed by extensively dialyzing, adding shuttle plasmid DNAs to Ad-pLys and allowing the complex formed by the shuttle plasmid wrapped around Ad-pLys to develop.

5 Fig. 11 is a schematic diagram of pCCL-DMD, which is described in detail in Example 9 below.

Fig. 12A - 12P provides the continuous DNA sequence of pAdΔ.CMVmDys [SEQ ID NO:10].

10 Detailed Description of the Invention

The present invention provides a unique recombinant adenovirus capable of delivering transgenes to target cells, as well as the components for production of the unique virus and methods for the use of the virus to
15 treat a variety of genetic disorders.

The AdΔ virus of this invention is a viral particle containing only the adenovirus cis-elements necessary for replication and virion encapsidation (i.e., ITRs and packaging sequences), but otherwise deleted of all
20 adenovirus genes (i.e., all viral open reading frames). This virus carries a selected transgene under the control of a selected promoter and other conventional regulatory components, such as a poly A signal. The AdΔ virus is characterized by improved persistence of the vector DNA
25 in the host cells, reduced antigenicity/immunogenicity, and hence, improved performance as a delivery vehicle. An additional advantage of this invention is that the AdΔ virus permits the packaging of very large transgenes, such as a full-length dystrophin cDNA for the treatment
30 of the progressive wasting of muscle tissue characteristic of Duchenne Muscular Dystrophy (DMD).

This novel recombinant virus is produced by use of an adenovirus-based vector production system containing two components: 1) a shuttle vector that comprises
35 adenovirus cis-elements necessary for replication and

virion encapsidation and is deleted of all viral genes, which vector carries a reporter or therapeutic minigene and 2) a helper adenovirus which, alone or with a packaging cell line, is capable of providing all of the viral gene products necessary for a productive viral infection when co-transfected with the shuttle vector. Preferably, the helper virus is modified so that it does not package itself efficiently. In this setting, it is desirably used in combination with a packaging cell line that stably expresses adenovirus genes. The methods of producing this viral vector from these components include both a novel means of packaging of an adenoviral/transgene containing vector into a virus, and a novel method for the subsequent separation of the helper virus from the newly formed recombinant virus.

I. The Shuttle Vector

The shuttle vector, referred to as pAdA, is composed of adenovirus sequences, and transgene sequences, including vector regulatory control sequences.

A. The Adenovirus Sequences

The adenovirus nucleic acid sequences of the shuttle vector provide the minimum adenovirus sequences which enable a viral particle to be produced with the assistance of a helper virus. These sequences assist in delivery of a recombinant transgene genome to a target cell by the resulting recombinant virus.

The DNA sequences of a number of adenovirus types are available from Genbank, including type Ad5 [Genbank Accession No. M73260]. The adenovirus sequences may be obtained from any known adenovirus serotype, such as serotypes 2, 3, 4, 7, 12 and 40, and further including any of the presently identified 41 human types [see, e.g., Horwitz, cited above]. Similarly adenoviruses known to infect other animals may also be employed in the

vector constructs of this invention. The selection of the adenovirus type is not anticipated to limit the following invention. A variety of adenovirus strains are available from the American Type Culture Collection, 5 Rockville, Maryland, or available by request from a variety of commercial and institutional sources. In the following exemplary embodiment an adenovirus, type 5 (Ad5) is used for convenience.

However, it is desirable to obtain a variety of 10 pAdA shuttle vectors based on different human adenovirus serotypes. It is anticipated that a library of such plasmids and the resulting AdA viral vectors would be useful in a therapeutic regimen to evade cellular, and possibly humoral, immunity, and lengthen the duration of 15 transgene expression, as well as improve the success of repeat therapeutic treatments. Additionally the use of various serotypes is believed to produce recombinant viruses with different tissue targeting specificities. The absence of adenoviral genes in the AdA viral vector 20 is anticipated to reduce or eliminate adverse CTL response which normally causes destruction of recombinant adenoviruses deleted of only the E1 gene.

Specifically, the adenovirus nucleic acid sequences employed in the pAdA shuttle vector of this 25 invention are adenovirus genomic sequences from which all viral genes are deleted. More specifically, the adenovirus sequences employed are the cis-acting 5' and 3' inverted terminal repeat (ITR) sequences of an adenovirus (which function as origins of replication) and 30 the native 5' packaging/enhancer domain, that contains sequences necessary for packaging linear Ad genomes and enhancer elements for the E1 promoter. These sequences are the sequences necessary for replication and virion encapsidation. See, e.g., P. Hearing et al, J. Virol., 35 61(8):2555-2558 (1987); M. Grable and P. Hearing, J.

Virol., 64(5): 2047-2056 (1990); and M. Grable and P. Hearing, J. Virol., 66(2):723-731 (1992).

According to this invention, the entire adenovirus 5' sequence containing the 5' ITR and packaging/enhancer region can be employed as the 5' adenovirus sequence in the pAdΔ shuttle vector. This left terminal (5') sequence of the Ad5 genome useful in this invention spans bp 1 to about 360 of the conventional adenovirus genome, also referred to as map units 0-1 of the viral genome. This sequence is provided herein as nucleotides 5496-5144 of SEQ ID NO: 1, nucleotides 600-958 of SEQ ID NO: 2; and nucleotides 9611-9254 of SEQ ID NO: 3, and generally is from about 353 to about 360 nucleotides in length. This sequence includes the 5' ITR (bp 1-103 of the adenovirus genome), and the packaging/enhancer domain (bp 194-358 of the adenovirus genome). See, Figs. 1A, 3, 5, and 7.

Preferably, this native adenovirus 5' region is employed in the shuttle vector in unmodified form. However, some modifications including deletions, substitutions and additions to this sequence which do not adversely effect its biological function may be acceptable. See, e.g., WO 93/24641, published December 9, 1993. The ability to modify these ITR sequences is within the ability of one of skill in the art. See, e.g., texts such as Sambrook et al, "Molecular Cloning. A Laboratory Manual.", 2d edit., Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (1989).

The 3' adenovirus sequences of the shuttle vector include the right terminal (3') ITR sequence of the adenoviral genome spanning about bp 35,353 - end of the adenovirus genome, or map units ~98.4-100. This sequence is provided herein as nucleotides 607-28 of SEQ ID NO: 1, nucleotides 16-596 of SEQ ID NO: 2; and nucleotides 3652-3073 of SEQ ID NO: 3, and generally is

about 580 nucleotides in length. This entire sequence is desirably employed as the 3' sequence of an pAdA shuttle vector. Preferably, the native adenovirus 3' region is employed in the shuttle vector in unmodified form.

5 However, some modifications to this sequence which do not adversely effect its biological function may be acceptable.

An exemplary pAdA shuttle vector of this invention, described below and in Fig. 2A, contains only
10 those adenovirus sequences required for packaging adenoviral genomic DNA into a preformed capsid head. The pAdA vector contains Ad5 sequences encoding the 5' terminal and 3' terminal sequences (identified in the description of Fig. 3), as well as the transgene
15 sequences described below.

From the foregoing information, it is expected that one of skill in the art may employ other equivalent adenovirus sequences for use in the AdA vectors of this invention. These sequences may include other adenovirus
20 strains, or the above mentioned cis-acting sequences with minor modifications.

B. The Transgene

The transgene sequence of the vector and recombinant virus is a nucleic acid sequence or reverse
25 transcript thereof, heterologous to the adenovirus sequence, which encodes a polypeptide or protein of interest. The transgene is operatively linked to regulatory components in a manner which permits transgene transcription.

30 The composition of the transgene sequence will depend upon the use to which the resulting virus will be put. For example, one type of transgene sequence includes a report r sequence, which upon expression produces a detectable signal. Such reporter sequences
35 include without limitation an *E. coli* beta-galactosidase

(LacZ) cDNA, a human placental alkaline phosphatase gene and a green fluorescent protein gene. These sequences, when associated with regulatory elements which drive their expression, provide signals detectable by conventional means, e.g., ultraviolet wavelength absorbance, visible color change, etc.

Another type of transgene sequence includes a therapeutic gene which expresses a desired gene product in a host cell. These therapeutic nucleic acid sequences typically encode products for administration and expression in a patient *in vivo* or *ex vivo* to replace or correct an inherited or non-inherited genetic defect or treat an epigenetic disorder or disease. Such therapeutic genes which are desirable for the performance of gene therapy include, without limitation, a normal cystic fibrosis transmembrane regulator (CFTR) gene (see Fig. 7), a low density lipoprotein (LDL) gene [T. Yamamoto et al, *Cell*, 39:27-28 (November, 1984)], a DMD cDNA sequence [partial sequences available from GenBank, Accession Nos. M36673, M36671, [A. P. Monaco et al, *Nature*, 323:646-650 (1986)] and L06900, [Roberts et al, *Hum. Mutat.*, 2:293-299 (1993)]] (Genbank), and a number of genes which may be readily selected by one of skill in the art. The selection of the transgene is not considered to be a limitation of this invention, as such selection is within the knowledge of the art-skilled.

C. Regulatory Elements

In addition to the major elements identified above for the pAdA shuttle vector, i.e., the adenovirus sequences and the transgene, the vector also includes conventional regulatory elements necessary to drive expression of the transgene in a cell transfected with the pAdA vector. Thus the vector contains a selected promoter which is linked to the transgene and located,

with the transgene, between the adenovirus sequences of the vector.

Selection of the promoter is a routine matter and is not a limitation of the pAdA vector itself.

- 5 Useful promoters may be constitutive promoters or regulated (inducible) promoters, which will enable control of the amount of the transgene to be expressed. For example, a desirable promoter is that of the cytomegalovirus immediate early promoter/enhancer [see, 10 e.g., Boshart et al, *Cell*, 41:521-530 (1985)]. This promoter is found at nucleotides 5117-4524 of SEQ ID NO: 1 and nucleotides 969-1563 of SEQ ID NO: 2. Another promoter is the CMV enhancer/chicken 8-actin promoter (nucleotides 9241-8684 of SEQ ID NO: 3). Another 15 desirable promoter includes, without limitation, the Rous sarcoma virus LTR promoter/enhancer. Still other promoter/enhancer sequences may be selected by one of skill in the art.

- The shuttle vectors will also desirably contain 20 nucleic acid sequences heterologous to the adenovirus sequences including sequences providing signals required for efficient polyadenylation of the transcript and introns with functional splice donor and acceptor sites (SD/SA). A common poly-A sequence which is employed in 25 the exemplary vectors of this invention is that derived from the papovavirus SV-40 [see, e.g., nucleotides 837-639 of SEQ ID NO: 1; 5245-5443 of SEQ ID NO: 2; and 3887-3684 of SEQ ID NO: 3]. The poly-A sequence generally is inserted in the vector following the transgene sequences and before the 3' adenovirus sequences. A common intron 30 sequence is also derived from SV-40, and is referred to as the SV-40 T intron sequence [see, e.g., nucleotides 4507-4376 of SEQ ID NO: 1 and 1579-1711 of SEQ ID NO: 2]. A pAdA shuttle vector of the present invention may also 35 contain such an intron, desirably located between the

promoter/enhancer sequence and the transgene. Selection of these and other common vector elements are conventional and many such sequences are available [see, e.g., Sambrook et al, and references cited therein].

- 5 Examples of such regulatory sequences for the above are provided in the plasmid sequences of Figs. 3, 5 and 7.

The combination of the transgene, promoter/enhancer, the other regulatory vector elements are referred to as a "minigene" for ease of reference herein.

- 10 The minigene is preferably flanked by the 5' and 3' cis-acting adenovirus sequences described above. Such a minigene may have a size in the range of several hundred base pairs up to about 30 kb due to the absence of adenovirus early and late gene sequences in the vector.
- 15 Thus, this AdA vector system permits a great deal of latitude in the selection of the various components of the minigene, particularly the selected transgene, with regard to size. Provided with the teachings of this invention, the design of such a minigene can be made by
- 20 resort to conventional techniques.

II. The Helper Virus

- Because of the limited amount of adenovirus sequence present in the AdA shuttle vector, a helper adenovirus of
- 25 this invention must, alone or in concert with a packaging cell line, provide sufficient adenovirus gene sequences necessary for a productive viral infection. Helper viruses useful in this invention thus contain selected adenovirus gene sequences, and optionally a second
- 30 reporter minigene.

- Normally, the production of a recombinant adenovirus which utilizes helper adenovirus containing a full complement of adenoviral genes results in recombinant virus contaminated by excess production of the helper
- 35 virus. Thus, extensive purification of the viral vector

from the contaminating helper virus is required. However, the present invention provides a way to facilitate purification and reduce contamination by crippling the helper virus.

5 One preferred embodiment of a helper virus of this invention thus contains three components (A) modifications or deletions of the native adenoviral gene sequences which direct efficient packaging, so as to substantially disable or "cripple" the packaging function
10 of the helper virus or its ability to replicate, (B) selected adenovirus genes and (C) an optional reporter minigene. These "crippled" helper viruses may also be formed into poly-cation conjugates as described below.

The adenovirus sequences forming the helper virus
15 may be obtained from the sources identified above in the discussion of the shuttle vector. Use of different Ad serotypes as helper viruses enables production of recombinant viruses containing the Δ Ad (serotype 5) shuttle vector sequences in a capsid formed by the other
20 serotype adenovirus. These recombinant viruses are desirable in targeting different tissues, or evading an immune response to the Δ Ad sequences having a serotype 5 capsid. Use of these different Ad serotype helper viruses may also demonstrate advantages in recombinant
25 virus production, stability and better packaging.

A. The Crippling Modifications

A desirable helper virus used in the production of the adenovirus vector of this invention is modified (or crippled) in its 5' ITR packaging/enhancer domain,
30 identified above. As stated above, the packaging/enhancer region contains sequences necessary for packaging linear adenovirus genomes ("PAC" sequences). More specifically, this sequence contains at least seven distinct yet functionally redundant domains

that are required for efficient encapsidation of replicated viral DNA.

Within a stretch of nucleotide sequence from bp 194-358 of the Ad5 genome, five of these so-called A-repeats or PAC sequences are localized (see, Fig. 1B). PAC I is located at bp 241-248 of the adenovirus genome (on the strand complementary to nucleotides 5259-5246 of SEQ ID NO: 1). PAC II is located at bp 262-269 of the adenovirus genome (on the strand complementary to nucleotides 5238-5225 of SEQ ID NO: 1). PAC III is located at bp 304-311 of the adenovirus genome (on the strand complementary to nucleotides 5196-5183 of SEQ ID NO: 1). PAC IV is located at bp 314-321 of the adenovirus (on the strand complementary to nucleotides 5186-5172 of SEQ ID NO: 1). PAC V is located at bp 339-346 of the adenovirus (on the strand complementary to nucleotides 5171-5147 of SEQ ID NO: 1).

Corresponding sequences can be obtained from SEQ ID NO: 2 and 3. PAC I is located at nucleotides 837-851 of SEQ ID NO: 2; and on the strand complementary to nucleotides 9374-9360 of SEQ ID NO: 3. PAC II is located at nucleotides 859-863 of SEQ ID NO: 2; and on the strand complementary to nucleotides 9353-9340 of SEQ ID NO: 3. PAC III is located at nucleotides 901-916 of SEQ ID NO: 2; and on the strand complementary to nucleotides 9311-9298 of SEQ ID NO: 3. PAC IV is located at nucleotides 911-924 of SEQ ID NO: 2; and on the strand complementary to nucleotides 9301-9288 of SEQ ID NO: 3. PAC V is located at nucleotides 936-949 of SEQ ID NO: 2; and on the strand complementary to nucleotides 9276-9263 of SEQ ID NO: 3.

Table 1 below lists these five native Ad5 sequences and a consensus PAC sequence based on the similarities between an eight nucleic acid stretch within the five sequences. The consensus sequence contains two positions at which the nucleic acid may be A or T (A/T). The conventional single letter designations are used for the nucleic acids, as is known to the art.

Table 1	
Adenovirus Genome Base Pair Nos. & <u>Nucleotide sequence</u>	
<u>A-Repeat</u>	
15 I	241 248 TAG TAAATTTG GGC [SEQ ID NO: 4]
20 II	262 269 AGT AAGATTTG GCC [SEQ ID NO: 5]
III	304 311 AGT GAAATCTG AAT [SEQ ID NO: 6]
25 IV	314 321 GAA TAATTTTG TGT [SEQ ID NO: 7]
V	339 346 CGT AATATTTG TCT [SEQ ID NO: 8]
30 Consensus 5' (A/T)AN(A/T)TTTG 3'	[SEQ ID NO: 9]

According to this invention, mutations or deletions may be made to one or more of these PAC sequences to generate desirable crippled helper viruses. A deletion analysis of the packaging domain revealed a positive correlation between encapsidation efficiency and the number of packaging A-repeats that were present at the 5' end of the genome. Modifications of this domain may include 5' adenovirus sequences which contain less than all five of the PAC sequences of Table 1. For example, only two PAC sequences may be present in the crippled virus, e.g., PAC I and PAC II, PAC III and PAC IV, and so on. Deletions of selected PAC sequences may

involve deletion of contiguous or non-contiguous sequences. For example, PAC II and PAC IV may be deleted, leaving PAC I, III and IV in the 5' sequence. Still an alternative modification may be the replacement of one or more of the native PAC sequences with one or more repeats of the consensus sequence of Table 1. Alternatively, this adenovirus region may be modified by deliberately inserted mutations which disrupt one or more of the native PAC sequences. One of skill in the art may further manipulate the PAC sequences to similarly achieve the effect of reducing the helper virus packaging efficiency to a desired level.

Exemplary helper viruses which involve the manipulation of the PAC sequences described above are disclosed in Example 7 below. Briefly, as described in that example, one helper virus contains in place of the native 5' ITR region (adenovirus genome bp 1-360), a 5' adenovirus sequence spanning adenovirus genome bp 1-269, which contains only the 5' ITR and PAC I and PAC II sequences, and deletes the adenovirus region bp 270-360.

Another PAC sequence modified helper virus contains only the 5' Ad5 sequence of the ITR and PAC I through PAC IV (Ad bp 1-321), deleting PAC V and other sequences in the Ad region bp322-360.

These modified helper viruses are characterized by reduced efficiency of helper virus encapsidation. These helper viruses with the specific modifications of the sequences related to packaging efficiency, provide a packaging efficiency high enough for generating production lots of the helper virus, yet low enough that they permit the achievement of higher yields of AdA transducing viral particles according to this invention.

B. The Selected Adenovirus Genes

Helper viruses useful in this invention, whether or not they contain the "crippling" modifications described above, contain selected adenovirus gene sequences depending upon the cell line which is transfected by the helper virus and shuttle vector. A preferred helper virus contains a variety of adenovirus genes in addition to the modified sequences described above.

As one example, if the cell line employed to produce the recombinant virus is not a packaging cell line, the helper virus may be a wild type Ad virus. Thus, the helper virus supplies the necessary adenovirus early genes E1, E2, E4 and all remaining late, intermediate, structural and non-structural genes of the adenovirus genome. This helper virus may be a crippled helper virus by incorporating modifications in its native 5' packaging/enhancer domain.

A desirable helper virus is replication defective and lacks all or a sufficient portion of the adenoviral early immediate early gene E1a (which spans mu 1.3 to 4.5) and delayed early gene E1b (which spans mu 4.6 to 11.2) so as to eliminate their normal biological functions. Such replication deficient viruses may also have crippling modifications in the packaging/enhancer domain. Because of the difficulty surrounding the absolute removal of adenovirus from AdA preparations that have been enriched by CsCl buoyant density centrifugation, the use of a replication defective adenovirus helper prevents the introduction of infectious adenovirus for *in vivo* animal studies. This helper virus is employed with a packaging cell line which supplies the deficient E1 proteins, such as the 293 cell line.

Additionally, all or a portion of the adenovirus delayed early gene E3 (which spans mu 76.6 to 86.2) may be eliminated from the adenovirus sequence which forms a part of the helper viruses useful in this invention, without adversely affecting the function of the helper virus because this gene product is not necessary for the formation of a functioning virus.

In the presence of other packaging cell lines which are capable of supplying adenoviral proteins in addition to the E1, the helper virus may accordingly be deleted of the genes encoding these adenoviral proteins.

Such additionally deleted helper viruses also desirably contain crippling modifications as described above.

C. A Reporter Minigene

It is also desirable for the helper virus to contain a reporter minigene, in which the reporter gene is desirably different from the reporter transgene contained in the shuttle vector. A number of such reporter genes are known, as referred to above. The presence of a reporter gene on the helper virus which is different from the reporter gene on the pAdA, allows both the recombinant AdA virus and the helper virus to be independently monitored. For example, the expression of recombinant alkaline phosphatase enables residual quantities of contaminating adenovirus to be monitored independent of recombinant LacZ expressed by an pAdA shuttle vector or an AdA virus.

D. Helper Virus Polycation Conjugates

Still another method for reducing the contamination of helper virus involves the formation of poly-cation helper virus conjugates, which may be associated with a plasmid containing other adenoviral genes, which are not present in the helper virus. The helper viruses described above may be further modified by resort to adenovirus-polylysine conjugate technology.

See, e.g., Wu et al, J. Biol. Chem., 264:16985-16987 (1989); and K. J. Fisher and J. M. Wilson, Biochem. J., 299: 49 (April 1, 1994), incorporated herein by reference.

5 Using this technology, a helper virus containing preferably the late adenoviral genes is modified by the addition of a poly-cation sequence distributed around the capsid of the helper virus. Preferably, the poly-cation is poly-lysine, which
10 attaches around the negatively-charged vector to form an external positive charge. A plasmid is then designed to express those adenoviral genes not present in the helper virus, e.g., the E1, E2 and/or E4 genes. The plasmid associates to the helper virus-conjugate through the
15 charges on the poly-lysine sequence. This modification is also desirably made to a crippled helper virus of this invention. This conjugate (also termed a trans-infection particle) permits additional adenovirus genes to be removed from the helper virus and be present on a plasmid
20 which does not become incorporated into the virus during production of the recombinant viral vector. Thus, the impact of contamination is considerably lessened.

25 **III. Assembly of Shuttle Vector, Helper Virus and
 Production of Recombinant Virus**

 The material from which the sequences used in the pAdΔ shuttle vector and the helper viruses are derived, as well as the various vector components and sequences employed in the construction of the shuttle vectors,
30 helper viruses, and AdΔ viruses of this invention, are obtained from commercial or academic sources based on previously published and described materials. These materials may also be obtained from an individual patient or generated and selected using standard recombinant
35 molecular cloning techniques known and practiced by those

skilled in the art. Any modification of existing nucleic acid sequences forming the vectors and viruses, including sequence deletions, insertions, and other mutations are also generated using standard techniques.

5 Assembly of the selected DNA sequences of the adenovirus, and the reporter genes or therapeutic genes and other vector elements into the pAdΔ shuttle vector using conventional techniques is described in Example 1 below. Such techniques include conventional cloning
10 techniques of cDNA such as those described in texts [Sambrook et al, cited above], use of overlapping oligonucleotide sequences of the adenovirus genomes, polymerase chain reaction, and any suitable method which provides the desired nucleotide sequence. Standard
15 transfection and co-transfection techniques are employed, e.g., CaPO₄ transfection techniques using the HEK 293 cell line. Other conventional methods employed in this invention include homologous recombination of the viral genomes, plaquing of viruses in agar overlay, methods of
20 measuring signal generation, and the like. Assembly of any desired AdΔ vector or helper virus of this invention is within the skill of the art, based on the teachings of this invention.

A. Shuttle Vector

25 As described in detail in Example 1 below and with resort to Fig. 2A and the DNA sequence of the plasmid reported in Fig. 3, a unique pAdΔ shuttle vector of this invention, pAdΔ.CMVLacZ, is generated. pAdΔ.CMVLacZ contains Ad5 sequences encoding the 5'
30 terminal followed by a CMV promoter/enhancer, a splice donor/splice acceptor sequence, a bacterial beta-galactosidase gene (LacZ), a SV-40 poly A sequence (pA), a 3' ITR from Ad5 and remaining plasmid sequence from plasmid pSP72 (Promega) backbone.

35

To generate the AdΔ genome which is incorporated in the vector, the plasmid pAdΔ.CMVLacZ must be must be digested with EcoRI to release the AdΔ.CMVLacZ genome, freeing the adenovirus ITRs and making them
5 available targets for replication. Thus production of the vector is "restriction-dependent", i.e., requires restriction endonuclease rescue of the replication template. See, Fig. 2B.

A second type of pAdΔ plasmid was designed
10 which places the 3' Ad terminal sequence in a head-to-tail arrangement relative to the 5' terminal sequence. As described in Example 1 and Figs. 4A, and with resort to the DNA sequence of the plasmid reported in Fig. 5, a second unique AdΔ vector sequence of this invention,
15 AdΔc.CMVLacZ, is generated from the shuttle plasmid pAdΔc.CMVLacZ, which contains an Ad5 5' ITR sequence and 3' ITR sequence positioned head-to-tail, followed by a CMV enhancer/ promoter, SD/SA sequence, LacZ gene and pA sequence in a plasmid pSP72 (Promega) backbone. As
20 described in Example 1B, this "restriction-independent" plasmid permits the AdΔ genome to be replicated and rescued from the plasmid backbone without including an endonuclease treatment (see, Fig. 4B).

B. Helper Virus

25 As described in detail in Example 2, an exemplary conventional E1 deleted adenovirus helper virus is virus Ad.CBhpAP, which contains a 5' adenovirus sequence from mu 0-1, a reporter minigene containing human placenta alkaline phosphatase (hpAP) under the
30 transcriptional control of the chicken β-actin promoter, followed by a poly-A sequence from SV40, followed by adenovirus sequences from 9.2 to 78.4 and 86 to 100. This helper contained deletions from mu 1.0 to 9.2 and 78.4 to 86, which eliminate substantially the E1 region
35 and the E3 region of the virus. This virus may be

desirably crippled according to this invention by modifications to its packaging enhancer domain.

Exemplary crippled helper viruses of this invention are described using the techniques described in Example 7 and contain the modified 5' PAC sequences, i.e., adenovirus genome bp 1-269; m.u. 0-0.75 or adenovirus genome bp 1-321; m.u. 0-0.89. Briefly, the 5' sequences are modified by PCR and cloned by conventional techniques into a conventional adenovirus based plasmid. A hpAP minigene is incorporated into the plasmid, which is then altered by homologous recombination with an E3 deleted adenovirus dl7001 to result in the modified vectors so that the reporter minigene is followed on its 3' end with the adenovirus sequences mu 9.6 to 78.3 and 87 to 100.

Generation of a poly-L-lysine conjugate helper virus was demonstrated essentially as described in detail in Example 5 below and Fig. 10 by coupling poly-L-lysine to the Ad.CBhpAP virion capsid. Alternatively, the same procedure may be employed with the PAC sequence modified helper viruses of this invention.

C. Recombinant AdA Virus

As stated above, a pAdA shuttle vector in the presence of helper virus and/or a packaging cell line permits the adenovirus-transgene sequences in the shuttle vector to be replicated and packaged into virion capsids, resulting in the recombinant AdA virus. The current method for producing such AdA virus is transfection-based and described in detail in Example 3. Briefly, helper virus is used to infect cells, such as the packaging cell line human HEK 293, which are then subsequently transfected with an pAdA shuttle vector containing a selected transgene by conventional methods. About 30 or more hours post-transfection, the cells are harvested, and an extract prepared. The AdA viral genome is

packaged into virions that sediment at a lower density than the helper virus in cesium gradients. Thus, the recombinant AdA virus containing a selected transgene is separated from the bulk of the helper virus by
5 purification via buoyant density ultracentrifugation in a CsCl gradient.

The yield of AdA transducing virus is largely dependent on the number of cells that are transfected with the pAdA shuttle plasmid, making it desirable to use
10 a transfection protocol with high efficiency. One such method involves use of a poly-L-lysinyated helper adenovirus as described above. A pAdA shuttle plasmid containing the desired transgene under the control of a suitable promoter, as described above, is then complexed
15 directly to the positively charged helper virus capsid, resulting in the formation of a single transfection particle containing the pAdA shuttle vector and the helper functions of the helper virus.

The underlying principle is that the helper
20 adenovirus coated with plasmid pAdA DNA will co-transport the attached nucleic acid across the cell membrane and into the cytoplasm according to its normal mechanism of cell entry. Therefore, the poly-L-lysine modified helper adenovirus assumes multiple roles in the context of an
25 AdA-based complex. First, it is the structural foundation upon which plasmid DNA can bind increasing the effective concentration. Second, receptor mediated endocytosis of the virus provides the vehicle for cell uptake of the plasmid DNA. Third, the endosomal activity associated with adenoviral infection facilitates
30 the release of internalized plasmid into the cytoplasm. And the adenovirus contributes trans helper functions on which the recombinant AdA virus is dependent for replication and packaging of transducing viral particles.
35 The Ad-based transfection procedure using an pAdA shuttle

vector and a polycation-helper conjugate is detailed in Example 6. Additionally, as described previously, the helper virus-plasmid conjugate may be another form of helper virus delivery of the omitted adenovirus genes not present in the pAdA vector. Such a structure enables the rest of the required adenovirus genes to be divided between the plasmid and the helper virus, thus reducing the self-replication efficiency of the helper virus.

A presently preferred method of producing the recombinant AdA virus of this invention involves performing the above-described transfection with the crippled helper virus or crippled helper virus conjugate, as described above. A "crippled" helper virus of this invention is unable to package itself efficiently, and therefor permits ready separation of the helper virus from the newly packaged AdA vector of this invention by use of buoyant density ultracentrifugation in a CsCl gradient, as described in the examples below.

IV. Function of the Recombinant AdA Virus

Once the AdA virus of this invention is produced by cooperation of the shuttle vector and helper virus, the AdA virus can be targeted to, and taken up by, a selected target cell. The selection of the target cell also depends upon the use of the recombinant virus, i.e., whether or not the transgene is to be replicated *in vitro* or *ex vivo* for production in a desired cell type for redelivery into a patient, or *in vivo* for delivery to a particular cell type or tissue. Target cells may be any mammalian cell (preferably a human cell). For example, in *in vivo* use, the recombinant virus can target to any cell type normally infected by adenovirus, depending upon the route of administration, i.e., it can target, without limitation, neurons, hepatocytes, epithelial cells and

the like. The helper adenovirus sequences supply the sequences necessary to permit uptake of the virus by the AdA.

Once the recombinant virus is taken up by a cell,
5 the adenovirus flanked transgene is rescued from the parental adenovirus backbone by the machinery of the infected cell, as with other recombinant adenoviruses. Once uncoupled (rescued) from the genome of the AdA virus, the recombinant minigene seeks an integration site
10 in the host chromatin and becomes integrated therein, either transiently or stably, providing expression of the accompanying transgene in the host cell.

V. Use of the AdA Viruses in Gene Therapy

15 The novel recombinant viruses and viral conjugates of this invention provide efficient gene transfer vehicles for somatic gene therapy. These viruses are prepared to contain a therapeutic gene in place of the LacZ reporter transgene illustrated in the exemplary
20 viruses and vectors. By use of the AdA viruses containing therapeutic transgenes, these transgenes can be delivered to a patient *in vivo* or *ex vivo* to provide for integration of the desired gene into a target cell. Thus, these viruses can be employed to correct genetic
25 deficiencies or defects. An example of the generation of an AdA gene transfer vehicle for the treatment of cystic fibrosis is described in Example 4 below. One of skill in the art can generate any number of other gene transfer vehicles by including a selected transgene for the
30 treatment of other disorders.

The recombinant viruses of the present invention may be administered to a patient, preferably suspended in a biologically compatible solution or pharmaceutically acceptable delivery vehicle. A suitable vehicle includes
35 sterile saline. Other aqueous and non-aqueous isotonic

30

sterile injection solutions and aqueous and non-aqueous sterile suspensions known to be pharmaceutically acceptable carriers and well known to those of skill in the art may be employed for this purpose.

5 The recombinant viruses of this invention may be administered in sufficient amounts to transfect the desired cells and provide sufficient levels of integration and expression of the selected transgene to provide a therapeutic benefit without undue adverse
10 effects or with medically acceptable physiological effects which can be determined by those skilled in the medical arts. Conventional and pharmaceutically acceptable parenteral routes of administration include direct delivery to the target organ, tissue or site,
15 intranasal, intravenous, intramuscular, subcutaneous, intradermal and oral administration. Routes of administration may be combined, if desired.

Dosages of the recombinant virus will depend primarily on factors such as the condition being treated,
20 the selected gene, the age, weight and health of the patient, and may thus vary among patients. A therapeutically effective human dosage of the viruses of the present invention is believed to be in the range of from about 20 to about 50 ml of saline solution
25 containing concentrations of from about 1×10^7 to 1×10^{10} pfu/ml virus of the present invention. A preferred human dosage is about 20 ml saline solution at the above concentrations. The dosage will be adjusted to balance the therapeutic benefit against any side effects. The
30 levels of expression of the selected gene can be monitored to determine the selection, adjustment or frequency of dosage administration.

35

The following examples illustrate the construction of the pAdΔ shuttle vectors, helper viruses and recombinant AdΔ viruses of the present invention and the use thereof in gene therapy. These examples are illustrative only, and do not limit the scope of the present invention.

Example 1 - Production of pAdΔ.CMVlacZ and pAdΔC.CMVlacZ Shuttle Vectors

10 A. pAdΔ.CMVlacZ

A human adenovirus Ad5 sequence was modified to contain a deletion in the E1a region [map units 1 to 9.2], which immediately follows the Ad 5' region (bp 1-360) (illustrated in Figs. 1A). Thus, the plasmid contains the 5' ITR sequence (bp 1-103), the native packaging/enhancer sequences and the TATA box for the E1a region (bp 104-360). A minigene containing the CMV immediate early enhancer/promoter, an SD/SA sequence, a cytoplasmic lacZ gene, and SV40 poly A (pA), was introduced at the site of the E1a deletion. This construct was further modified so that the minigene is followed by the 3' ITR sequences (bp 35,353-end). The DNA sequences for these components are provided in Fig. 3 and SEQ ID NO: 1 (see, also the brief description of this figure).

This construct was then cloned by conventional techniques into a pSP72 vector (Promega) backbone to make the circular shuttle vector pAdΔCMVlacZ. See the schematic of Fig. 2A. This construct was engineered with EcoRI sites flanking the 5' and 3' Ad5 ITR sequences. pAdΔ.CMVlacZ was then subjected to enzymatic digestion with EcoRI, releasing a linear fragment of the vector spanning the terminal end of the Ad 5' ITR sequence through the terminal end of the 3' ITR sequence from the plasmid backbone. See Fig. 2B.

B. pAdΔC.CMVlacZ

The shuttle vector pAdΔC.CMVlacZ (Figs. 4A and 5) was constructed using a pSP72 (Promega) backbone so that the Ad5 5' ITR and 3' ITR were positioned head-to-tail. The organization of the Ad5 ITRs was based on reports that suggest circular Ad genomes that have the terminal ends fused together head-to-tail are infectious to levels comparable to linear Ad genomes. A minigene encoding the CMV enhancer, an SD/SA sequence, the LacZ gene, and the poly A sequence was inserted immediately following the 5' ITR. The DNA sequence of the resulting plasmid and the sequences for the individual components are reported in Fig. 5 and SEQ ID NO: 2 (see also, brief description of Fig. 5). This plasmid does not require enzymatic digestion prior to its use to produce the viral particle (see Example 3). This vector was designed to enable restriction-independent production of LacZ AdΔ vectors.

20 Example 2 - Construction of a Helper Virus

The Ad.CBhpAP helper virus [K. Kozarsky et al, Som. Cell Mol. Genet., 19(5):449-458 (1993)] is a replication deficient adenovirus containing an alkaline phosphatase minigene. Its construction involved conventional cloning and homologous recombination techniques. The adenovirus DNA substrate was extracted from CsCl purified d17001 virions, an Ad5 (serotype subgroup C) variant that carries a 3 kb deletion between mu 78.4 through 86 in the nonessential E3 region (provided by Dr. William Wold, Washington University, St. Louis, Missouri). Viral DNA was prepared for co-transfection by digestion with ClaI (adenovirus genomic bp position 917) which removes the left arm of the genome encompassing adenovirus map units 0-2.5. See lower diagram of Fig. 1B.

A parental cloning vector, pAd.BglII was designed. It contains two segments of wild-type Ad5 genome (i.e., map units 0-1 and 9-16.1) separated by a unique BglII cloning site for insertion of heterologous sequences.

- 5 The missing Ad5 sequences between the two domains (adenovirus genome bp 361-3327) results in the deletion of Ela and the majority of Elb following recombination with viral DNA.

- A recombinant hpAP minigene was designed and
10 inserted into the BglII site of pAd.BglII to generate the complementing plasmid, pAdCBhpAP. The linear arrangement of this minigene includes:

- (a) the chicken cytoplasmic β -actin promoter [nucleotides +1 to +275 as described in T. A. Kost et al, 15 Nucl. Acids Res., 11(23):8287 (1983); nucleotides 9241-8684 of Fig. 7];

- (b) an SV40 intron (e.g., nucleotides 1579-1711 of SEQ ID NO: 2),

- (c) the sequence for human placental alkaline
20 phosphatase (available from Genbank) and

- (d) an SV40 polyadenylation signal (a 237 Bam HI-BclI restriction fragment containing the cleavage/poly-A signals from both the early and late transcription units; e.g., nucleotides 837-639 of SEQ ID NO: 1).

- 25 The resulting complementing plasmid, pAdCBhpAP contained a single copy of recombinant hpAP minigene flanked by adenovirus coordinates 0-1 on one side and 9.2-16.1 on the other.

- Plasmid DNA was linearized using a unique NheI site
30 immediately 5' to adenovirus map unit zero (0) and the above-identified adenovirus substrate and the complementing plasmid DNAs were transfected to 293 cells [ATCC CRL1573] using a standard calcium phosphate transfection procedure [see, e.g., Sambrook et al, cited
35 above]. The end result of homologous recombination

involving sequences that map to adenovirus map units 9-16.1 is hybrid Ad.CBhpAP helper virus which contains adenovirus map units 0-1 and, in place of the E1a and E1b coding regions from the dl7001 adenovirus substrate, is the hpAP minigene from the plasmid, followed by Ad sequences 9 to 100, with a deletion in the E3 (78.4-86 mu) regions.

Example 3 - Production of Recombinant AdA Virus

The recombinant AdA virus of this invention are generated by co-transfection of a shuttle vector with the helper virus in a selected packaging or non-packaging cell line.

As described in detail below, the linear fragment provided in Example 1A, or the circular AdA genome carrying the LacZ of Example 1B, is packaged into the Ad.CBhpAP helper virus (Example 2) using conventional techniques, which provides an empty capsid head, as illustrated in Fig. 2C. Those virus particles which have successfully taken up the pAd shuttle genome into the capsid head can be distinguished from those containing the hpAP gene by virtue of the differential expression of LacZ and hpAP.

In more detail, 293 cells (4×10^7 pfu 293 cells/150 mm dish) were seeded and infected with helper virus Ad.CBhpAP (produced as described in Example 2) at an MOI of 5 in 20 ml DMEM/2% fetal bovine serum (FBS). This helper specific marker is critical for monitoring the level of helper virus contamination in AdA preparations before and after purification. The helper virus provides in trans the necessary helper functions for synthesis and packaging of the AdΔCMVLacZ genome.

Two hours post infection, using either the restriction-dependent shuttle vector or the restriction-independent shuttle vector, plasmid pAdΔ.CMVLacZ

(digested with *ScorI*) or pAdAc.CMVlacZ DNA, each carrying a LacZ minigene, was added to the cells by a calcium phosphate precipitate (2.5 ml calcium phosphate transfection cocktail containing 50 µg plasmid DNA).

- 5 Thirty to forty hours post-transfection, cells were harvested, suspended in 10 mM Tris-Cl (pH 8.0) (0.5 ml/150 mm plate) and frozen at -80°C. Frozen cell suspensions were subjected to three rounds of freeze (ethanol-dry ice)-thaw (37°C) cycles to release virion capsids. Cell debris was removed by centrifugation (5,000xg for 10 minutes) and the clarified supernatant applied to a CsCl gradients to separate recombinant virus from helper virus as follows.
- 10

- Supernatants (10 ml) applied to the discontinuous CsCl gradient (composed of equal volumes of CsCl at 1.2 g/ml, 1.36 g/ml, and 1.45 g/ml 10 mM Tris-Cl (pH 8.0)) were centrifuged for 8 hours at 72,128Xg, resulting in separation of infectious helper virus from incompletely formed virions. Fractions were collected from the interfacing zone between the helper and top components and analyzed by Southern blot hybridization or for the presence of LacZ transducing particles. For functional analysis, aliquots (2.0 ml from each sample) from the same fractions were added to monolayers of 293 cells (in 35 mm wells) and expression of recombinant β -galactosidase determined 24 hours later. More specifically, monolayers were harvested, suspended in 0.3 ml 10 mM Tris-Cl (pH 8.0) buffer and an extract prepared by three rounds of freeze-thaw cycles. Cell debris was removed by centrifugation and the supernatant tested for β -galactosidase (LacZ) activity according to the procedure described in J. Price et al, Proc. Natl. Acad. Sci., USA, 84:156-160 (1987). The specific activity (milliunits β -galactosidase/mg protein or reporter
- 15
- 20
- 25
- 30

enzymes was measured from indicator cells. For the recombinant virus, specific activity was 116.

Fractions with β -galactosidase activity from the discontinuous gradient were sedimented through an equilibrium cesium gradient to further enrich the preparation for AdA virus. A linear gradient was generated in the area of the recombinant virus spanning densities 1.29 to 1.34gm/ml. A sharp peak of the recombinant virus, detected as the appearance of the β -gal activity in infected 293 cells, eluted between 1.31 and 1.33 gm/dl. This peak of recombinant virus was located between two major A_{260} nm absorbing peaks and in an area of the gradient with the helper virus was precipitously dropping off. The equilibrium sedimentation gradient accomplished another 102 to 103 fold purification of recombinant virus from helper virus. The yield of recombinant AdA.CMVlacZ virus recovered from a 50 plate prep after 2 sedimentations ranged from 107 to 108 transducing particles.

Analysis of lysates of cells transfected with the recombinant vector and infected with helper revealed virions capable of transducing the recombinant minigene contained within the vector. Subjecting aliquots of the fractions to Southern analysis using probes specific to the recombinant virus or helper virus revealed packaging of multiple molecular forms of vector derived sequence. The predominant form of the deleted viral genome was the size (~5.5 kb) of the corresponding double stranded DNA monomer (AdA.CMVlacZ) with less abundant but discrete higher molecular weight species (~10 kb and ~15 kb) also present. Full-length helper virus is 35kb. Importantly, the peak of vector transduction activity corresponds with the highest molecular weight form of the deleted virus. These results confirm the hypothesis that ITRs and contiguous packaging sequence are the only elements

necessary for incorporation into virions. An apparently ordered or preferred rearrangement of the recombinant Ad monomer genome leads to a more biologically active molecule. The fact that larger molecular species of the
5 deleted genome are 2x and 3x as large as the monomer deleted virus genome suggests that the rearrangements may involve sequential duplication of the original genome.

These same procedures may be adapted for production of a recombinant AdA virus using a crippled helper virus
10 or helper virus conjugate as described previously.

Example 4 - Recombinant AdA Virus Containing a
Therapeutic Minigene

To test the versatility of the recombinant AdA virus
15 system, the reporter LacZ minigene obtained from pAdA-CMV-LacZ was cassette replaced with a therapeutic minigene encoding CFTR.

The minigene contained human CFTR cDNA [Riordan et al, Science, 245:1066-1073 (1989); nucleotides 8622-4065
20 of SEQ ID NO: 3] under the transcriptional control of a chimeric CMV enhancer/chicken β -actin promoter element (nucleotides +1 to +275 as described in T. A. Kost et al, Nucl. Acids Res., 11(23):8287 (1983); nucleotides 9241-8684 of SEQ ID NO: 3, Fig. 7); and followed by an SV-40
25 poly-A sequence (nucleotides 3887-3684 of SEQ ID NO: 3, Fig. 7).

The CFTR minigene was inserted into the E1 deletion site of an Ad5 virus (called pAd.E1A) which contains a deletion in E1a from mu 1-9.2 and a deletion in E3 from
30 mu 78.4-86.

The resulting shuttle vector called pAdA.CBCFTR (see Figs. 6 and the DNA sequence of Fig. 7 [SEQ ID NO: 3]) used the same Ad ITRs of pAdA-CMV-LacZ, but the Ad5 sequences terminated with NheI sites instead of EcoRI.

Therefore release of the minigene from the plasmid was accomplished by digestion with NheI.

The vector production system described in Example 3 was employed, using the helper virus Ad.CBhpAP (Example 2). Monolayers of 293 cells grown to 80-90% confluency in 150 mm culture dishes were infected with the helper virus at an MOI of 5. Infections were done in DMEM supplemented with 2% FBS at 20 ml media/150 mm plate. Two hours post-infection, 50 µg plasmid DNA in 2.5 ml transfection cocktail was added to each plate and evenly distributed.

Delivery of the pAdΔ.CBCFTR plasmid to 293 cells was mediated by formation of a calcium phosphate precipitate and AdΔ.CBCFTR virus resolved from Ad.CBhpAP helper virus by CsCl buoyant density ultracentrifugation as follows:

Cells were left in this condition for 10-14 h, after which the infection/transfection media was replaced with 20 ml fresh DMEM/2% FBS. Approximately 30 h post-transfection, cells were harvested, suspended in 10 mM Tris-Cl (pH 8.0) buffer (0.5 ml/150 mm plate), and stored at -80°C.

Frozen cell suspensions were lysed by three sequential rounds of freeze (ethanol-dry ice)-thaw (37°C). Cell debris was removed by centrifugation (5,000 x g for 10 min) and 10 ml clarified extract layered onto a CsCl step gradient composed of three 9.0 ml tiers with densities 1.45 g/ml, 1.36 g/ml, and 1.20 g/ml CsCl in 10 mM Tris-Cl (pH 8.0) buffer. Centrifugation was performed at 20,000 rpm in a Beckman SW-28 rotor for 8 h at 4°C. Fractions (1.0 ml) were collected from the bottom of the centrifuge tube and analyzed for rAd transducing vectors. Peak fractions were combined and banded to equilibrium. Fractions containing transducing virions were dialyzed against 20 mM HEPES (pH 7.8)/150 mM NaCl

(HBS) and stored frozen at -80°C in the presence of 10% glycerol or as a liquid stock at -20°C (HBS+40% glycerol).

Fractions collected after ultracentrifugation were analyzed for transgene expression and vector DNA. For lacZ ArAd vectors, 2 μl aliquots were added to 293 cell monolayers seeded in 35 mm culture wells. Twenty-four hours later cells were harvested, suspended in 0.3 ml 10 mM Tris-Cl (pH 8.0) buffer, and lysed by three rounds of freeze-thaw. Cell debris was removed by centrifugation (15,000 x g for 10 min) and assayed for total protein [Bradford, (1976)] and β -galactosidase activity [Sambrook et al, (1989)] using ONPG (o-Nitrophenyl β -D-galactopyranoside) as substrate.

Expression of CFTR protein from the AdA.CBCFTR vector was determined by immunofluorescence localization. Aliquots of AdA.CBCFTR, enriched by two-rounds of ultracentrifugation and exchanged to HBS storage buffer, were added to primary cultures of airway epithelial cells obtained from the lungs of CF transplant recipients. Twenty-four hours after the addition of vector, cells were harvested and affixed to glass slides using centrifugal force (Cytospin 3, Shandon Scientific Limited). Cells were fixed with freshly prepared 3% paraformaldehyde in PBS (1.4 mM KH_2PO_4 , 4.3 mM Na_2HPO_4 , 2.7 mM KCl, and 137 mM NaCl) for 15 min at room temperature (RT), washed twice in PBS, and permeabilized with 0.05% NP-40 for 10 min at RT. The immunofluorescence procedure began with a blocking step in 10% goat serum (PBS/GS) for 1 h at RT, followed by binding of the primary monoclonal mouse anti-human CFTR (R-domain specific) antibody (Genzyme) diluted 1:500 in PBS/GS for 2 h at RT. Cells were washed extensively in PBS/GS and incubated for 1 h at RT with a donkey anti-mouse IgG (H+L) FITC conjugated

antibody (Jackson ImmunoResearch Laboratories) diluted 1:100 in PBS/GS.

For Southern analysis of vector DNA, 5 μ l aliquots were taken directly from CsCl fractions and incubated
5 with 20 μ l capsid digestion buifer (50 mM Tris-Cl, pH 8.0; 1.0 mM EDTA, pH 8.0; 0.5% SDS, and 1.0 mg/ml Proteinase K) at 50°C for 1 h. The reactions were allowed to cool to RT, loading dye was added, and electrophoresed through a 1.2% agarose gel. Resolved
10 DNAs were electroblotted onto a nylon membrane (Hybond-N) and hybridized with a 32-P labeled restriction fragment. Blots were analyzed by autoradiography or scanned on a Phosphorimager 445 SI (Molecular Dynamics).

The results that were obtained from Southern blot
15 analysis of gradient fractions revealed a distinct viral band that migrated faster than the helper Ad.CBhpAP DNA. The highest viral titers mapped to fractions 3 and 4. Quantitation of the bands in fraction 4 indicated the titer of Ad.CBhpAP was approximately 1.5x greater than
20 Ad Δ CBCFTR. However, if the size difference between the two viruses is factored in (Ad.CBhpAP=35 kb; Ad Δ CBCFTR=6.2 kb), the viral titer (where 1 particle=1 DNA molecule) of Ad Δ CB.CFTR is at least 4-fold greater than the viral titer of Ad.CBhpAP.

25 While Southern blot analysis of gradient fractions was useful for showing the production of Ad Δ viral particles, it also demonstrated the utility of ultracentrifugation for purifying Ad Δ viruses. Considering the latter of these, both LacZ and CFTR
30 transducing viruses banded in CsCl to an intermediate density between infectious adenovirus helper virions (1.34 g/ml) and incompletely formed capsids (1.31 g/ml). The lighter density relative to helper virus likely results from the smaller genome carried by the Ad Δ
35 viruses. This further suggests changes in virus size

influences the density and purification of AdA virus. Regardless, the ability to separate AdA virus from the helper virus is an important observation and suggests further purification may be achieved by successive rounds of banding through CsCl.

This recombinant virus is useful in gene therapy alone, or preferably, in the form of a conjugate prepared as described herein.

Example 5 - Correction of Genetic Defect in CF airway Epithelial Cells with AdACB.CFTR

Treatment of cystic fibrosis, utilizing the recombinant virus provided above, is particularly suited for *in vivo*, lung-directed, gene therapy. Airway epithelial cells are the most desirable targets for gene transfer because the pulmonary complications of CF are usually its most morbid and life-limiting.

The recombinant AdACB.CFTR virus was fractionated on sequential CsCl gradients and fractions containing CFTR sequences, migrating between the adenovirus and top components fractions described above were used to infect primary cultures of human airway epithelial cells derived from the lungs of a CF patient. The cultures were subsequently analyzed for expression of CFTR protein by immunocytochemistry. Immunofluorescent detection with mouse anti-human CFTR (R domain specific) antibody was performed 24 hours after the addition of the recombinant virus. Analysis of mock infected CF cells failed to reveal significant binding to the R domain specific CFTR antibody. Primary airway epithelium cultures exposed to the recombinant virus demonstrated high levels of CFTR protein in 10-20% of the cells.

Thus, the recombinant virus of the invention, containing the CFTR gene, may be delivered directly into the airway, e.g. by a formulating the virus above, into a

preparation which can be inhaled. For example, the recombinant virus or conjugate of the invention containing the CFTR gene, is suspended in 0.25 molar sodium chloride. The virus or conjugate is taken up by respiratory airway cells and the gene is expressed.

Alternatively, the virus or conjugates of the invention may be delivered by other suitable means, including site-directed injection of the virus bearing the CFTR gene. In the case of CFTR gene delivery, preferred solutions for bronchial instillation are sterile saline solutions containing in the range of from about 1×10^7 to 1×10^{10} pfu/ml, more particularly, in the range of from about 1×10^8 to 1×10^9 pfu/ml of the virus of the present invention.

Other suitable methods for the treatment of cystic fibrosis by use of gene therapy recombinant viruses of this invention may be obtained from the art discussions of other types of gene therapy vectors for CF. See, for example, U. S. Patent No. 5,240,846, incorporated by reference herein.

Example 6 - Synthesis of Polycation Helper Virus Conjugate

Another version of the helper virus of this invention is a polylysine conjugate which enables the pAdΔ shuttle plasmid to complex directly with the helper virus capsid. This conjugate permits efficient delivery of shuttle plasmid pAdΔ shuttle vector in tandem with the helper virus, thereby removing the need for a separate transfection step. See, Fig. 10 for a diagrammatic outline of this construction. Alternatively, such a conjugate with a plasmid supplying some Ad genes and the helper supplying the remaining necessary genes for production of the AdΔ viral vector provides a novel way

to reduce contamination of the helper virus, as discussed above.

Purified stocks of a large-scale expansion of Ad.CBhpAP were modified by coupling poly-L-lysine to the virion capsid essentially as described by K. J. Fisher and J. M. Wilson, Biochem. J., 299:49-58 (1994), resulting in an Ad.CBhpAP-(Lys)_n conjugate. The procedure involves three steps.

First, CsCl band purified helper virus Ad.CBhpAP was reacted with the heterobifunctional crosslinker sulfo-SMCC [sulfo-(N-succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate] (Pierce). The conjugation reaction, which contained 0.5 mg (375 nmol) of sulpho-SMCC and 6×10^{12} A₂₆₀ helper virus particles in 3.0 ml of HBS, was incubated at 30°C for 45 minutes with constant gentle shaking. This step involved formation of a peptide bond between the active N-hydroxysuccinimide (NHS) ester of sulpho-SMCC and a free amine (e.g. lysine) contributed by an adenovirus protein sequence (capsid protein) in the vector, yielding a maleimide-activated viral particle. The activated adenovirus is shown in Fig. 10 having the capsid protein fiber labeled with the nucleophilic maleimide moiety. In practice, other capsid polypeptides including hexon and penton base are also targeted.

Unincorporated, unreacted cross-linker was removed by gel filtration on a 1 cm x 15 cm Bio-Gel P-6DG (Bio-Rad Laboratories) column equilibrated with 50 mM Tris/HCl buffer, pH 7.0, and 150 mM NaCl. Peak A₂₆₀ fractions containing maleimide-activated helper virus were combined and placed on ice.

Second, poly-L-lysine having a molecular mass of 58 kDa at 10 mg/ml in 50 mM triethanolamine buffer (pH 8.0), 150 mM NaCl and 1 mM EDTA was thiolated with 2-iminothiolane/HCl (Traut's Reagent; Pierce) to a molar

ratio of 2 moles-SH/mole polylysine under N_2 ; the cyclic thioimide reacts with the poly(L-lysine) primary amines resulting in a thiolated polycation. After a 45 minute incubation at room temperature the reaction was applied to a 1 cm x 15 cm Bio-Gel P6DG column equilibrated with 50 mM Tris/HCl buffer (pH 7.0), 150 mM NaCl and 2 mM EDTA to remove unincorporated Traut's Reagent.

Quantification of free thiol groups was accomplished with Ellman's reagent [5,5'-dithio-bis-(2-nitrobenzoic acid)], revealing approximately 3-4 mol of -SH/mol of poly(L-lysine). The coupling reaction was initiated by adding 1×10^{12} A_{260} particles of maleimide-activated helper virus/mg of thiolated poly(L-lysine) and incubating the mixture on ice at 4°C for 15 hours under argon. 2-mercaptoethylamine was added at the completion of the reaction and incubation carried out at room temperature for 20 minutes to block unreacted maleimide sites.

Virus-polylysine conjugates, Ad.CPAP-p(Lys)_n, were purified away from unconjugated poly(L-lysine) by ultracentrifugation through a CsCl step gradient with an initial composition of equal volumes of 1.45 g/ml (bottom step) and 1.2 g/ml (top step) CsCl in 10 mM Tris/HCl buffer (pH 8.0). Centrifugation was at 90,000 g for 2 hours at 5°C. The final product was dialyzed against 20 mM Hepes buffer (pH 7.8) containing 150 mM NaCl (HBS).

Example 7 - Formation of AdA/helper-pLys Viral Particle

The formation of Ad.CBhpAP-pLys/pAdA.CMVlacZ particle is initiated by adding 20 μ g plasmid pAdA.CMVlacZ DNAs to 1.2×10^{12} A_{260} particles Ad.CBhpAP-pLys in a final volume of 0.2 ml DMEM and allowing the complex to develop at room temperature for between 10-15 minutes. This ratio typically represents the plasmid DNA binding capacity of a standard lot of adenovirus-pLys

conjugate and gives the highest levels of plasmid transgene expression.

The resulting trans-infection particle is transfected onto 293 cells (4×10^7 cells seeded on a 150 mm dish). Thirty hours after transfection, the particles are recovered and subjected to a freeze/thaw technique to obtain an extract. The extract is purified on a CsCl step gradient with gradients at 1.20 g/ml, 1.36 g/ml and 1.45 g/ml. After centrifugation at 90,000 x g for 8 hours, the AdA vectors were obtained from a fraction under the top components as identified by the presence of LacZ, and the helper virus was obtained from a smaller, denser fraction, as identified by the presence of hpAP.

Example 8 - Construction of Modified Helper Viruses with Crippled Packaging (PAC) Sequences

This example refers to Figs. 9A through 9C, 10A and 10B in the design of modified helper viruses of this invention.

Ad5 5' terminal sequences that contained PAC domains I and II (Fig. 8A) or PAC domains I, II, III, and IV (Fig. 8B) were generated by PCR from the wild type Ad5 5' genome depicted in Fig. 1B using PCR clones indicated by the arrows in Fig. 1B. The resulting amplification products (Fig. 8A and 8B) sequences differed from the wild-type Ad5 genome in the number of A-repeats carried by the left (5') end.

As depicted in Fig. 8C, these amplification products were subcloned into the multiple cloning site of pAd.Link.1 (IHGT Vector Core). pAd.Link.1 is a adenovirus based plasmid containing adenovirus m.u. 9.6 through 16.1. The insertion of the modified PAC regions into pAd.Link.1 generated two vectors pAd.PACII (containing PAC domains I and II) and pAd.PACIV (c ntaining PAC domains I, II, III, and IV).

Thereafter, as depicted in Figs. 10A and 10B, for each of these plasmids, a human placenta alkaline phosphatase reporter minigene containing the immediate early CMV enhancer/promoter (CMV), human placenta alkaline phosphatase cDNA (hpa1), and SV40 polyadenylation signal (pA), was subcloned into each PAC vector, generating pAd.PACII.CMVhpAP and pAd.PACIV.CMVhpAP, respectively.

These plasmids were then used as substrates for homologous recombination with dl7001 virus, described above, by co-transfection into 293 cells. Homologous recombination occurred between the adenovirus map units 9-16 of the plasmid and the crippled Ad5 virus. The results of homologous recombination were helper viruses containing Ad5 5' terminal sequences that contained PAC domains I and II or PAC domains I, II, III, and IV, followed by the minigene, and Ad5 3' sequences 9.6-78.3 and 87-100. Thus, these crippled viruses are deleted of the E1 gene and the E3 gene.

The plaque formation characteristics of the PAC helper viruses gave an immediate indication that the PAC modifications diminished the rate and extent of growth. Specifically, PAC helper virus plaques did not develop until day 14-21 post-transfection, and on maturation remained small. From previous experience, a standard first generation Ad.CBhpAP helper virus with a complete left terminal sequence would begin to develop by day 7 and mature by day 10.

Viral plaques were picked and suspended in 0.5 ml of DMEM media. A small aliquot of the virus stock was used to infect a fresh monolayer of 293 cells and histochemically stained for recombinant alkaline phosphatase activity 24 hours post-infection. Six of eight Ad.PACIV.CMVhpAP (encodes A-repeats I-IV) clones that were screened for transgene expression were

positive, while all three Ad.PACII.CMVhpAP clones that were selected scored positive. The clones have been taken through two rounds of plaque purification and are currently being expanded to generate a working stock.

5 These crippled helper viruses are useful in the production of the AdA virus particles according to the procedures described in Example 3. They are characterized by containing sufficient adenovirus genes to permit the packaging of the shuttle vector genome, but
10 their crippled PAC sequences reduce their efficiency for self-encapsidation. Thus less helper viruses are produced in favor of more AdA recombinant viruses. Purification of AdA virus particles from helper viruses is facilitated in the CsCl gradient, which is based on
15 the weight of the respective viral particles. This facility in purification is a decided advantage of the AdA vectors of this invention in contrast to adenovirus vectors having only E1 or smaller deletions. The AdA vectors even with minigenes of up to about 15 kb are
20 significantly different in weight than wild type or other adenovirus helpers containing many adenovirus genes.

Example 9 - AdA Vector Containing a full-length dystrophin transgene

25 Duchenne muscular dystrophy (DMD) is a common x-linked genetic disease caused by the absence of dystrophin, a 427K protein encoded by a 14 kilobase transcript. Lack of this important sarcolemmal protein leads to progressive muscle wasting, weakness, and death.
30 One current approach for treating this lethal disease is to transfer a functional copy of the dystrophin gene into the affected muscles. For skeletal muscle, a replication-defective adenovirus represents an efficient delivery system.

According to the present invention, a recombinant plasmid pAdΔ.CMVmdys was created which contains only the Ad5 cis-elements (i.e., ITRs and contiguous packaging sequences) and harbors the full-length murine dystrophin gene driven by the CMV promoter. This plasmid was generated as follows.

pSL1180 [Pharmacia Biotech] was cut with Not I, filled in by Klenow, and religated thus ablating the Not I site in the plasmid. The resulting plasmid is termed pSL1180NN and carries a bacterial ori and Amp resistance gene.

pAdΔ.CMVLacZ of Example 1 was cut with EcoRI, klenowed, and ligated with the ApaI-cut pSL1180NN to form pAdΔ.CMVLacZ (ApaI).

The 14 kb mouse dystrophin cDNA [sequences provided in C. C. Lee et al, Nature, 349:334-336 (1991)] was cloned in two large fragments using a lambda ZAP cloning vector (Stratagene) and subsequently cloned into the bluescript vector pSK- giving rise to the plasmid pCCL-DMD. A schematic diagram of this vector is provided in Fig. 11, which illustrates the restriction enzyme sites.

pAdΔ.CMVLacZ (ApaI) was cut with NotI and the large fragment gel isolated away from the lacZ cDNA. pCCL-DMD was also cut with NotI, gel isolated and subsequently ligated to the large NotI fragment of NotI digested pAdΔ.CMVLacZ (ApaI). The sequences of resulting vector, pAdΔ.CMVmdys, are provided in Fig. 12A-12P [SEQ ID NO:10].

This plasmid contains sequences from the left-end of the Ad5 encompassing bp 1-360 (5' ITR), a mouse dystrophin minigene under the control of the CMV promoter, and sequence from the right end of Ad5 spanning

bp 35353 to the end of the genome (3' ITR). The minigene is followed by an SV-40 poly-A sequence similar to that described for the plasmids described above.

The vector production system described herein is employed. Ten 150mm 293 plates are infected at about 90% confluency with a reporter recombinant E1-deleted virus Ad.CBhpAP at an MOI of 5 for 60 minutes at 37°C. These cells are transfected with pAdΔ.CMVmDys by calcium phosphate co-precipitation using 50 μg linearized DNA/dish for about 12-16 hours at 37°C. Media is replaced with DMEM + 10% fetal bovine serum.

Full cytopathic effect is observed and a cell lysate is made by subjecting the cell pellet to freeze-thaw procedures three times. The cells are subjected to an SW41 three tier CsCl gradient for 2 hours and a band migrating between the helper adenovirus and incomplete virus is detected.

Fractions are assayed on a 6 well plate containing 293 cells infected with 5λ of fraction for 16-20 hours in DMEM + 2% FBS. Cells are collected, washed with phosphate buffered saline, and resuspended in 2 ml PBS. 200λ of the 2ml cell fractions is cytospun onto a slide.

The cells were subjected to immunofluorescence for dystrophin as follows. Cells were fixed in 10N MeOH at -20°C. The cells were exposed to a monoclonal antibody specific for the carboxy terminus of human dystrophin [NCL-DYS2; Novocastra Laboratories Ltd., UK]. Cells were then washed three times and exposed to a secondary antibody, i.e. 1:200 goat anti-mouse IgG in FITC.

The titer/fraction for seven fractions revealed in the immunofluorescent stains were calculated by the following formula and reported in Table 2 below.
$$\text{DFU/field} = (\text{DFU}/200\lambda \text{ cells}) \times 10 = \text{DFU}/10^6 \text{ cells} =$$
$$(\text{DFU}/5\lambda \text{ viral fraction}) \times 20 = \text{DFU}/100\lambda \text{ fraction}.$$

Table 2

	<u>Fraction</u>	<u>DFU/100λ</u>
5	1	--
	2	--
	3	6×10^3
10	4	1.8×10^4
	5	9.6×10^3
15	6	200
	7	200

A virus capable of transducing the dystrophin minigene is detected as a "positive" (i.e., green fluorescent) cell. The results of the IF illustrate that heat-treated fractions do not show positive immunofluorescence. Southern blot data suggest one species on the same size as the input DNA, with helper virus contamination.

The recombinant virus can be subsequently separated from the majority of helper virus by sedimentation through cesium gradients. Initial studies demonstrate that the functional AdCMVΔmDys virions are produced, but are contaminated with helper virus. Successful purification would render AdΔ virions that are incapable of encoding viral proteins but are capable of transducing murine skeletal muscle.

Example 10 - Pseudotyping

The following experiment provides a method for preparing a recombinant AdΔ according to the invention, utilizing helper viruses from serotypes which differ from that of the pAdΔ in the transfection/infection protocol. It is unexpected that the ITRs and packaging sequence of

Ad5 could be incorporated into a virion of another serotype.

A. Protocol

The basic approach is to transfect the
5 AdΔ.CMVlacZ recombinant virus (Ad5) into 293 cells and subsequently infect the cell with the helper virus derived from a variety of Ad serotypes (2, 3, 4, 5, 7, 8, 12, and 40). When CPE is achieved, the lysate is harvested and banded through two cesium gradients.

10 More particularly, the Ad5-based plasmid pAdΔ.CMVlacZ of Example 1 was linearized with EcoRI. The linearized plasmids were then transfected into ten 150 mm dishes of 293 cells using calcium phosphate co-precipitation. At 10-15 hours post transfection, wild
15 type adenoviruses (of one of the following serotypes: 2, 3, 4, 5, 7, 12, 40) were used to infect cells at an MOI of 5. The cells were then harvested at full CPE and lysed by three rounds of freeze-thawing. Pellet is resuspended in 4 mL Tris-HCl. Cell debris was removed by
20 centrifugation and partial purification of Ad5Δ.CMVlacZ from helper virus was achieved with 2 rounds of CsCl gradient centrifugation (SW41 column, 35,000 rpm, 2 hours). Fractions were collected from the bottom of the tube (fraction #1) and analysed for lacZ transducing
25 viruses on 293 target cells by histochemical staining (at 20h PI). Contaminating helper viruses were quantitated by plaque assay.

Except for adenovirus type 3, infection with Ad serotypes 2, 4, 5, 7, 12 and 40 were able to produce lacZ
30 transducing viruses. The peak of β-galactosidase activity was detected between the two major A₂₆₀ absorbing peaks, where most of the helper viruses banded (data not shown). The quantity of lacZ virus recovered from 10 plates ranged from 10⁴ to 10⁸ transducing
35 particles depending on the serotype of the helper. As

expected Ad2 and Ad5 produced the highest titer of *lacZ* transducing viruses (Table 3). Wild type contamination was in general 10^2 - 10^3 log higher than corresponding *lacZ* titer except in the case of Ad40.

5 B. Results

Table 3 summarizes the growth characteristics of the wild type adenoviruses as evaluated on propagation in 293 cells. This demonstrated the feasibility of utilizing these helper viruses to infect the cell line
10 which has been transfected with the Ad5 deleted virus.

Table 3

Adenovirus serotypes	p/ml	pfu/ml	p:pfu
15 2	5×10^{12}	2.5×10^{11}	20:01
3	1×10^{12}	6.25×10^9	160:1
20 4	3×10^{12}	2×10^9	150:1
5	1×10^{12}	5×10^{10}	20:01
25 7a	5×10^{12}	1×10^{11}	50:1
12	6×10^{11}	4×10^9	150:1
35	1.2×10^{12}		
30 40	2.2×10^{12}	4.4×10^8	5000:1

Table 4 summarizes the results of the final purified fractions. The middle column, labeled LFU/ μ l
35 quantifies the production of *lacZ* forming units, which is a direct measure of the packaging and propagation of pseudotyped recombinant Ad Δ virus. The pfu/ μ l titer is an estimate of the contaminating wild type virus. Ad Δ virus pseudotyped with all adenoviral strains was
40 generated except for Ad3. The titers range between 10^7 - 10^4 .

53

Table 4

	Serotypes	LFU/ml	PFU/ml
5	2	4.6×10^7	1.8×10^9
	3	0	NA
10	4	6.7×10^6	9.3×10^7
	5	6.3×10^7	1.9×10^9
	7a	3×10^6	1.8×10^8
15	12	1.2×10^5	3.3×10^8
	40	9.5×10^4	1.5×10^3
20			

Table 5A-5D represents a more detailed analysis of the fractions from the second purification for each of the experiments summarized in Table 4. Again, LFU/ μ l is the recovery of the AdA viruses, whereas pfu/ μ l represents recovery of the helper virus.

Table 5A

	Ad2 Fraction #	VOLUME/ μ l	LFU/ μ l	PFU/ μ l
30	1	120	9532	8×10^6
	2	100	5.8×10^4	3×10^6
35	3	100	8.24×10^4	6×10^5
	4	100	9.47×10^4	1.2×10^5
40	5	100	6×10^4	8×10^4
	6	100	2×10^4	6×10^4
	7	100	5434	5×10^4
45	Total/10 pH		3.32×10^7	1.35×10^9

50

Table 5B

5	Ad4 Fraction #	VOLUME/ul	LFU/ul	PFU/ul
10	1	100	1000	1.75×10^5
	2	100	1.79×10^4	2.8×10^5
	3	100	1.8×10^4	5.5×10^4
15	4	100	2909	1.25×10^4
	5	100	920	4×10^4
20	6	100	153	3×10^3
	Total/10 pH		4×10^6	5.6×10^7
25	Ad5 Fraction #			
	1	120	1.98×10^4	6×10^6
30	2	100	5.8×10^4	3×10^6
	3	100	1.2×10^5	1.5×10^6
	4	100	1×10^5	1.4×10^5
35	5	100	7.96×10^4	8×10^4
	6	100	6860	6×10^4
40	Total/10 pH		3.88×10^7	1.2×10^9

Table 5C

5	Ad7 Fraction #	VOLUME/ul	LFU/ul	PFU/ul
	1	100	1225	5×10^5
10	2	100	5550	4×10^5
	3	100	4938	2×10^5
	4	100	3866	8×10^4
15	5	100	4134	6×10^4
	6	100	995	7×10^4
	7	100	230	6×10^3
20	Total/10 pH		2.09×10^6	1.3×10^8
25	Ad12 Fraction #			
	1	100	31	5×10^5
	2	80	169	8.5×10^5
30	3	80	245	1.8×10^5
	4	110	161	1.1×10^5
35	5	120	62	7×10^3
	Total/10 pH		6.14×10^4	1.65×10^8

56

Table 5D

	Ad40 Fraction #	VOLUME/ul	LFU/ul	PFU/ul
5	1	80	61	5
	2	80	184	3
10	3	80	199	3
	4	80	168	1
	5	80	122	
15	6	100	46	
	7	100	32	
20	Total/10 pH		6.65×10^4	1.1×10^3

C. Characterization of the Structure of Packaged25 Viruses

Aliquots of serial fractions were analysed by Southern blots using *lacZ* as a probe. In the case of Ad2 and 5, not only the linearized monomer was packaged but multiple forms of recombinant virus with distinct sizes were found. These forms correlated well with the sizes of dimers, trimers and other higher molecular weight concatamers. The linearized monomers peaked closer to the top of tube (the defective adenovirus band) than other forms. When these forms were correlated with *lacZ* activity, a better correlation was found between the higher molecular weight forms than the monomers. With pseudotyping of Ad4 and Ad7, no linearized monomers were packaged and only higher molecular weight forms were found.

40 These data definitively demonstrate the production and characterization of the Δ virus and the different pseudotypes. This example illustrates a very simple way of generating pseudotype viruses.

Example 11 - AdA Vector Containing a FH Gene

Familial hypercholesterolemia (FH) is an autosomal dominant disorder caused by abnormalities (deficiencies) in the function or expression of LDL receptors [M.S. Brown and J.L. Goldstein, Science, 232(4746):34-37 (1986); J.L. Goldstein and M.S. Brown, "Familial hypercholesterolemia" in Metabolic Basis of Inherited Disease, ed. C.R. Scriver et al, McGraw Hill, New York, pp1215-1250 (1989).] Patients who inherit one abnormal allele have moderate elevations in plasma LDL and suffer premature life-threatening coronary artery disease (CAD). Homozygous patients have severe hypercholesterolemia and life-threatening CAD in childhood. An FH-containing vector of the invention is constructed by replacing the lacZ minigene in the pAdA.CMVlacZ vector with a minigene containing the LDL receptor gene [T. Yamamoto et al, Cell, 39:27-38 (1984)] using known techniques and as described analogously for the dystrophin gene and CFTR in the preceding examples. Vectors bearing the LDL receptor gene can be readily constructed according to this invention. The resulting plasmid is termed pAdA.CMV-LDL.

This plasmid is useful in gene therapy of FH alone, or preferably, in the form of a conjugate prepared as described herein to substitute a normal LDL gene for the abnormal allele responsible for the gene.

A. Ex Vivo Gene Therapy

Ex vivo gene therapy can be performed by harvesting and establishing a primary culture of hepatocytes from a patient. Known techniques may be used to isolate and transduce the hepatocytes with the above vector(s) bearing the LDL receptor gene(s). For example, techniques of collagenase perfusion developed for rabbit liver can be adapted for human tissue and used in transduction. Following transduction, the hepatocytes

are removed from the tissue culture plates and reinfused into the patient using known techniques, e.g. via a catheter placed into the inferior mesenteric vein.

B. In Vivo Gene Therapy

5 Desirably, the *in vivo* approach to gene therapy, e.g. liver-directed, involves the use of the vectors and vector conjugates described above. A preferred treatment involves infusing a vector LDL conjugate of this invention into the peripheral
10 circulation of the patient. The patient is then evaluated for change in serum lipids and liver tissues.

The virus or conjugate can be used to infect hepatocytes *in vivo* by direct injection into a peripheral or portal vein (10^7 - 10^8 pfu/kg) or retrograde into the
15 biliary tract (same dose). This effects gene transfer into the majority of hepatocytes.

Treatments are repeated as necessary, e.g. weekly. Administration of a dose of virus equivalent to an MOI of approximately 20 (i.e. 20 pfu/hepatocyte) is
20 anticipated to lead to high level gene expression in the majority of hepatocytes.

All references recited above are incorporated herein by reference. Numerous modifications and variations of the present invention are included in the above-
25 identified specification and are expected to be obvious to one of skill in the art. Such modifications and alternations to the compositions and processes of the present invention, such as various modifications to the PAC sequences or the shuttle vectors, or to other
30 sequences of the vector, helper virus and minigene components, are believed to be encompassed in the scope of the claims appended hereto.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Trustees of the University of Pennsylvania
Wilson, James M.
Fisher, Krishna J.
Chen, Shu-Jen
Weitzman, Matthew
- (ii) TITLE OF INVENTION: Improved Adenovirus and Methods
of Use Thereof
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Howson and Howson
 - (B) STREET: Spring House Corporate Cntr, PO Box 457
 - (C) CITY: Spring House
 - (D) STATE: Pennsylvania
 - (E) COUNTRY: USA
 - (F) ZIP: 19477
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/331,381
 - (B) FILING DATE: 28-OCT-1994
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Bak, Mary E.
 - (B) REGISTRATION NUMBER: 31,215
 - (C) REFERENCE/DOCKET NUMBER: GNVPN.008PCT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 215-540-9200
 - (B) TELEFAX: 215-540-5818

60

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTATGTGTTG GGAATTGTAG TTTTCTTAAA ATGGGAAGTT ACGTAACGTG	200
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TTCTGGGCGT AGGTTCGCGT GCGGTTTTCT GGGTGTTTTT TGTGGACTTT	300
AACCGTTACG TCATTTTTTA GTCCTATATA TACTCGCTCT GCACTTGGCC	350
CTTTTTTACA CTGTGACTGA TTGAGCTGGT GCCGTGTCGA GTGGTGTTTT	400
TTTAATAGGT TTTCTTTTTT ACTGGTAAGG CTGACTGTTA GGCTGCCGCT	450
GTGAAGCGCT GTATGTTGTT CTGGAGCGGG AGGGTGCTAT TTTGCCTAGG	500
CAGGAGGGTT TTTCAGGTGT TTATGTGTTT TTCTCTCCTA TTAATTTTGT	550
TATACCTCCT ATGGGGGCTG TAATGTTGTC TCTACGCCTG CGGGTATGTA	600
TTCCCCCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCGAAAAA	650
ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA TGCAATTGTT	700
GTTGTAACT TGTTTATTGC AGCTTATAAT GGTACAAAT AAAGCAATAG	750
CATCACAAAT TTCACAAATA AAGCATTTTT TCACTGCAT TCTAGTTGTG	800
GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT CCCC GCGGCC	850
GCCTAGAGTC GAGGCCGAGT TTGTCAGAAA GCAGACCAA CAGCGGTTGG	900
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GGTCAAAACA	GGCGGCAGTA	AGGCGGTCGG	GATAGTTTTTC	TTGCGGCCCT	1500
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GGTAATGGCC	CGCCGCCCTC	CAGCGTTCGA	CCCAGGCGTT	AGGGTCAATG	1800
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TCGTTATCGC	TATGACGGAA	CAGGTATTCG	CTGGTCACTT	CGATGGTTTTG	2300

62

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TTTCAATATT	GGCTTCATCC	ACCACATACA	GGCCGTAGCG	GTGCGACAGC	3000
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GTTGTTCTGC	TTCATCAGCA	GGATATCCTG	CACCATCGTC	TGCTCATCCA	3100
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TGTTGGGAAG	GGCGATCGGT	GCGGGCCTCT	TCGCTATTAC	GCCAGCTGGC	4100
CAAAGGGGGA	TGTGCTGCAA	GGCGATTAAAG	TTGGGTAACG	CCAGGGTTTT	4150
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64

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ACCCGCCCCG	TTCCCACGCC	CCGCGCCACG	TCACAACTC	CACCCCCTCA	5450
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AGTAAACTTG	GTCTGACAGT	TACCAATGCT	TAATCAGTGA	GGCACCTATC	6600
TCAGCGATCT	GTCTATTTCT	TTCATCCATA	GTTGCCTGAC	TCCCCGTCGT	6650
GTAGATAACT	ACGATACGGG	AGGGCTTACC	ATCTGGCCCC	AGTGCTGCAA	6700
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TCGGTCCTCC	GATCGTTGTC	AGAAGTAAGT	TGGCCGCAGT	GTTATCACTC	7050
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ATGCTTTTCT	GTGACTGGTG	AGTACTCAAC	CAAGTCATTC	TGAGAATAGT	7150
GTATGCGGCG	ACCAGATTGC	TCTTGCCCGG	CGTCAATACG	GGATAATACC	7200
GCGCCACATA	GCAGAACTTT	AAAAGTGCTC	ATCATTGGAA	AACGTTCTTC	7250
GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT	GTTGAGATCC	AGTTCGATGT	7300
AACCCACTCG	TGCACCCAAC	TGATCTTCAG	CATCTTTTAC	TTTCACCAGC	7350
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ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA	TGAGCGGATA	CATATTTGAA	7500

66

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CAGAACAACA TACAGCGCTT CACAGCGGCA GCCTAACAGT CAGCCTTACC	200
AGTAAAAAAG AAAACCTATT AAAAAACAC CACTCGACAC GGCACCAGCT	250
CAATCAGTCA CAGTGTA AAAA AAGGGCCAAG TGCAGAGCGA GTATATATAG	300
GACTAAAAAA TGACGTAACG GTTAAAGTCC AAAAAAACA CCCAGAAAAC	350
CGCACGCGAA CCTACGCCCA GAAACGAAAG CAAAAAACC CAACTTCC	400
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67

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CATCATCAAT	AATATACCTT	ATTTTGGATT	GAAGCCAATA	TGATAATGAG	650
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TAGTAGTGTG	GCGGAAGTGT	GATGTTGCAA	G ₁ GTGGCGGA	ACACATGTAA	750
GCGACGGATG	TGGCAAAAGT	GACGTTTTTG	GTGTGCGCCG	GTGTACACAG	800
GAAGTGACAA	TTTTCGCGCG	GTTTTAGGCG	GATGTTGTAG	TAAATTTGGG	850
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AGTACGCCCC	CTATTGACGT	CAATGACGGT	AAATGGCCCG	CCTGGCATT A	1200
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68

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TATCGCTGGA	TCAAATCTGT	CGATCCTTCC	C ₆ CCCGGTGC	AGTATGAAGG	3350
CGGCGGAGCC	GACACCACGG	CCACCGATAT	TATTTGCCCG	ATGTACGCGC	3400
GCGTGGATGA	AGACCAGCCC	TTCCCGGCTG	TGCCGAAATG	GTCCATCAAA	3450
AAATGGCTTT	CGCTACCTGG	AGAGACGCGC	CCGCTGATCC	TTTGCGAATA	3500
CGCCCACGCG	ATGGGTAAAC	GTCCTGGCGG	TTTCGCTAAA	TACTGGCAGG	3550
CGTTTCGTCA	GTATCCCCGT	TTACAGGGCG	GCTTCGTCTG	GGACTGGGTG	3600
GATCAGTCGC	TGATTAAATA	TGATGAAAAC	GGCAACCCGT	GGTCGGCTTA	3650
CGGCGGTGAT	TTTGGCGATA	CGCCGAACGA	TCGCCAGTTC	TGTATGAACG	3700
GTCTGGTCTT	TGCCGACCGC	ACGCCGCATC	CAGCGCTGAC	GGAAGCAAAA	3750
CACCAGCAGC	AGTTTTTCCA	GTTCCGTTTA	TCCGGGCAAA	CCATCGAAGT	3800
GACCAGCGAA	TACCTGTTCC	GTCATAGCGA	TAACGAGCTC	CTGCACTGGA	3850
TGGTGGCGCT	GGATGGTAAG	CCGCTGGCAA	GCGGTGAAGT	GCCTCTGGAT	3900
GTGCTCCAC	AAGGTAAACA	GTTGATTGAA	CTGCCTGAAC	TACCGCAGCC	3950
GGAGAGCGCC	GGGCAACTCT	GGCTCACAGT	ACGCGTAGTG	CAACCGAACG	4000
CGACCGCATG	GTCAGAAGCC	GGGCACATCA	GCGCCTGGCA	GCAGTGGCGT	4050
CTGGCGGAAA	ACCTCAGTGT	GACGCTCCCC	GCCGCGTCCC	ACGCCATCCC	4100
GCATCTGACC	ACCAGCGAAA	TGGATTTTTG	CATCGAGCTG	GGTAATAAGC	4150
GTTGGCAATT	TAACCGCCAG	TCAGGCTTTC	TTTCACAGAT	GTGGATTGGC	4200
GATAAAAAAC	AACTGCTGAC	GCCGCTGCGC	GATCAGTTCA	CCCGTGCACC	4250
GCTGGATAAC	GACATTGGCG	TAAGTGAAGC	GACCCGCATT	GACCCTAACG	4300
CCTGGGTCGA	ACGCTGGAAG	GCGGCGGGCC	ATTACCAGGC	CGAAGCAGCG	4350
TTGTTGCAGT	GCACGGCAGA	TACACTTGCT	GATGCGGTGC	TGATTACGAC	4400
CGCTCACGCG	TGGCAGCATC	AGGGGAAAAC	CTTATTTATC	AGCCGGAAAA	4450

70

CCTACCGGAT	TGATGGTAGT	GGTCAAATGG	CGATTACCGT	TGATGTTGAA	4500
GTGGCGAGCG	ATACACCGCA	TCCGGCGCGG	ATTGGCCTGA	ACTGCCAGCT	4550
GGCGCAGGTA	GCAGAGCGGG	TAAACTGGCT	CGGATTAGGG	CCGCAAGAAA	4600
ACTATCCCGA	CCGCCTTACT	GCCGCCTGTT	TTGACCGCTG	GGATCTGCCA	4650
TTGTCAGACA	TGTATACCCC	GTACGTCTTC	CCGAGCGAAA	ACGGTCTGCG	4700
CTGCGGGACG	CGCGAATTGA	ATTATGGCCC	ACACCAGTGG	CGCGGCGACT	4750
TCCAGTTCAA	CATCAGCCGC	TACAGTCAAC	AGCAACTGAT	GGAAACCAGC	4800
CATCGCCATC	TGCTGCACGC	GGAAGAAGGC	ACATGGCTGA	ATATCGACGG	4850
TTTCCATATG	GGGATTGGTG	GCGACGACTC	CTGGAGCCCG	TCAGTATCGG	4900
CGGAATTACA	GCTGAGCGCC	GGTCGCTACC	ATTACCAGTT	GGTCTGGTGT	4950
CAAAAATAAT	AATAACCGGG	CAGGCCATGT	CTGCCCGTAT	TTCGCGTAAG	5000
GAAATCCATT	ATGTACTATT	TAAAAAACAC	AAACTTTTGG	ATGTTCGGTT	5050
TATTCTTTTT	CTTTTACTTT	TTTATCATGG	GAGCCTACTT	CCCGTTTTTC	5100
CCGATTTGGC	TACATGACAT	CAACCATATC	AGCAAAAGTG	ATACGGGTAT	5150
TATTTTTTGC	GCTATTTCTC	TGTTCTCGCT	ATTATTCCAA	CCGCTGTTTG	5200
GTCTGCTTTC	TGACAAACTC	GGCCTCGACT	CTAGGCGGCC	GCGGGGATCC	5250
AGACATGATA	AGATACATTG	ATGAGTTTGG	ACAAACCACA	ACTAGAATGC	5300
AGTGAAAAAA	ATGCTTTATT	TGTGAAATTT	GTGATGCTAT	TGCTTTATTT	5350
GTAACCATTA	TAAGCTGCAA	TAAACAAGTT	AACAACAACA	ATTGCATTCA	5400
TTTTATGTTT	CAGGTTCAGG	GGGAGGTGTG	GGAGGTTTTT	TCGGATCCTC	5450
TAGAGTCGAC	GACGCGAGGC	TGGATGGCCT	TCCCCATTAT	GATTCTTCTC	5500
GCTTCCGGCG	GCATCGGGAT	GCCCCGCTTG	CAGGCCATGC	TGTCCAGGCA	5550
GGTAGATGAC	GACCATCAGG	GACAGCTTCA	AGGATCGCTC	GCGGCTCTTA	5600
CCAGCCTAAC	TTCGATCACT	GGACCGCTGA	TCGTACGGC	GATTTATGCC	5650
GCCTCGGCGA	GCACATGGAA	CGGGTTGGCA	TGGATTGTAG	GCGCCGCCCT	5700
ATACCTTGTC	TGCCTCCCCG	CGTTGCGTCG	CGGTGCATGG	AGCCGGGCCA	5750

CCTCGACCTG	AATGGAAGCC	GGCGGCACCT	CGCTAACGGA	TTCACCACTC	5800
CAAGAATTGG	AGCCAATCAA	TTCTTGCGGA	GAAGTGTGAA	TGCGCAAACC	5850
AACCCTTGGC	AGAACATATC	CATCGCGTCC	GCCATCTCCA	GCAGCCGCAC	5900
GCGGCGCATC	TCGGGCAGCG	TTGGGTCCTG	GJCACGGGTG	CGCATGATCG	5950
TGCTCCTGTC	GTTGAGGACC	CGGCTAGGCT	GGCGGGGTTG	CCTTACTGGT	6000
TAGCAGAATG	AATCACCGAT	ACGCGAGCGA	ACGTGAAGCG	ACTGCTGCTG	6050
CAAAACGTCT	GCGACCTGAG	CAACAACATG	AATGGTCTTC	GGTTTCCGTG	6100
TTTCGTAAAG	TCTGGAACG	CGGAAGTCAG	CGCCCTGCAC	CATTATGTTC	6150
CGGATCTGCA	TCGCAGGATG	CTGCTGGCTA	CCCTGTGGAA	CACCTACATC	6200
TGTATTAACG	AAGCCTTTCT	CAATGCTCAC	GCTGTAGGTA	TCTCAGTTCTG	6250
GTGTAGGTCG	TTGCTCCAA	GCTGGGCTGT	GTGCACGAAC	CCCCCGTTCA	6300
GCCCCACCGC	TGCGCCTTAT	CCGGTAACTA	TCGTCTTGAG	TCCAACCCGG	6350
TAAGACACGA	CTTATCGCCA	CTGGCAGCAG	CCACTGGTAA	CAGGATTAGC	6400
AGAGCGAGGT	ATGTAGGCGG	TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	6450
CTACGGCTAC	ACTAGAAGGA	CAGTATTTGG	TATCTGCGCT	CTGCTGAAGC	6500
CAGTTACCTT	CGGAAAAAGA	GTTGGTAGCT	CTTGATCCGG	CAAACAAACC	6550
ACCGCTGGTA	GCGGTGGTTT	TTTTGTTTGC	AAGCAGCAGA	TTACGCGCAG	6600
AAAAAAAGGA	TCTCAAGAAG	ATCCTTTGAT	CTTTTCTACG	GGGTCTGACG	6650
CTCAGTGGA	CGAAACTCA	CGTTAAGGGA	TTTTGGTCAT	GAGATTATCA	6700
AAAAGGATCT	TCACCTAGAT	CCTTTTAAAT	TAAAAATGAA	GTTTAAATC	6750
AATCTAAAGT	ATATATGAGT	AAACTTGTC	TGACAGTTAC	CAATGCTTAA	6800
TCAGTGAGGC	ACCTATCTCA	GCGATCTGTC	TATTTGTTTC	ATCCATAGTT	6850
GCCTGACTCC	CCGTCGTGTA	GATAACTACG	ATACGGGAGG	GCTTACCATC	6900
TGGCCCCAGT	GCTGCAATGA	TACCGCGAGA	CCCACGCTCA	CCGGCTCCAG	6950
ATTTATCAGC	AATAAACAG	CCAGCCGGA	GGGCCGAGCG	CAGAAGTGGT	7000
CCTGCAACTT	TATCCGCCTC	CATCCAGTCT	ATTAATTGTT	GCCGGGAAGC	7050

72

TAGAGTAAGT	AGTTCGCCAG	TTAATAGTTT	GCGCAACGTT	GTTGCCATTG	7100
CTGCAGGCAT	CGTGGTGTCA	CGCTCGTCGT	TTGGTATGGC	TTCATTTCAGC	7150
TCCGGTTCCC	AACGATCAAG	GCGAGTTACA	TCATCCCCCA	TGTTGTGCAA	7200
AAAAGCGGTT	AGCTCCTTCG	GTCCTCCGAT	CGTTGTGAGA	AGTAAGTTGG	7250
CCGCAGTGTT	ATCACTCATG	GTTATGCCAG	CACTGCATAA	TTCTCTTACT	7300
GTCATGCCAT	CCGTAAGATG	CTTTTCTGTG	ACTGGTGAGT	ACTCAACCAA	7350
GTCATTCTGA	GAATAGTGTA	TGCGGCGACC	GAGTTGCTCT	TGCCCCGGCGT	7400
CAACACGGGA	TAATACCGCG	CCACATAGCA	CAACTTTAAA	AGTGCTCATC	7450
ATTGGA AAAAC	GTTCTTCGGG	GCGAAAAC TC	TCAAGGATCT	TACCGCTGTT	7500
GAGATCCAGT	TCGATGTAAC	CCACTCGTGC	ACCCAACTGA	TCTTCAGCAT	7550
CTTTTACTTT	CACCAGCGTT	TCTGGGTGAG	CAAAAACAGG	AAGGCAAAAAT	7600
GCCGCAAAAA	AGGGAATAAG	GGCGACACGG	AAATGTTGAA	TACTCATACT	7650
CTTCCTTTTT	CAATATTATT	GAAGCATTTA	TCAGGGTTAT	TGTCTCATGA	7700
GCGGATACAT	ATTTGAATGT	ATTTAGAAAA	ATAAACAAAT	AGGGGTTCCG	7750
CGCACATTTC	CCCGAAAAGT	GCCACCTGAC	GTCTAAGAAA	CCATTATTAT	7800
CATGACATTA	ACCTATAAAA	ATAGGCGTAT	CACGAGGCCC	TTTCGTCTTC	7850
AA					7852

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	CGCTCGGTGC	TTCGGCTGCG	50
GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	TCCACAGAAT	100

CAGGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAGGCC	150
AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTCCATA GGCTCCGCCC	200
CCCTGACGAG CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC	250
CGACAGGACT ATAAAGATAC CAGGCGTTTC CCCTGGAAG CTCCCTCGTG	300
CGCTCTCCTG TTCCGACCCT GCCGCTTACC GGATACCTGT CCGCCTTTCT	350
CCCTTCGGGA AGCGTGGCGC TTTCTCATAG CTCACGCTGT AGGTATCTCA	400
GTTCGGTGTA GGTGCTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC	450
GTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA	500
CCCGGTAAGA CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA	550
TTAGCAGAGC GAGGTATGTA GCGGTGCTA CAGAGTTCTT GAAGTGGTGG	600
CCTAACTACG GCTACACTAG AAGAACAGTA TTTGGTATCT GCGCTCTGCT	650
GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA TCCGGCAAAC	700
AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG	750
CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGGTC	800
TGACGCTCAG TGGAACGAAA ACTCACGTTA AGGGATTTTG GTCATGAGAT	850
TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTAAAA ATGAAGTTTT	900
AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG	950
CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA	1000
TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA	1050
CCATCTGGCC CCAGTGCTGC AATGATACCG CCAGACCCAC GCTCACCGGC	1100
TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA	1150
GTGGTCTGTC AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG	1200
GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC	1250
CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT	1300
TCAGCTCCGC TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG	1350
TGCAAAAAG CGGTTAGCTC CTTGCGTCCT CCGATCGTTG TCAGAAGTAA	1400

74

GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC	1450
TTACTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA	1500
ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC	1550
GGCGTCAATA CGGGATAATA CCGCGCCACA TAGCAGAACT TAAAAAGTGC	1600
TCATCATTTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG	1650
CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC	1700
AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC	1750
AAAATGCCGC AAAAAAGGGA ATAAGGGCGA CACGGAAATG TTGAATACTC	1800
ATACTCTTCC TTTTTC AATA TTATTGAAGC ATTTATCAGG GTTATTGTCT	1850
CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGGGG	1900
TTCCGCGCAC ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCATT	1950
ATTATCATGA CATTAACTA TAAAAATAGG CGTATCACGA GGCCCTTTTCG	2000
TCTCGCGCGT TTCGGTGATG ACGGTGAAAA CCTCTGACAC ATGCAGCTCC	2050
CGGAGACGGT CACAGCTTGT CTGTAAGCGG ATGCCGGGAG CAGACAAGCC	2100
CGTCAGGGCG CGTCAGCGGG TGTTGGCGGG TGTCGGGGCT GGCTTAACTA	2150
TGCGGCATCA GAGCAGATTG TACTGAGAGT GCACCATAAA ATTGTAAACG	2200
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TTTAACCAAT AGGCCGAAAT CGGCAAAATC CCTTATAAAT CAAAAGAATA	2300
GCCCAGATA GGGTTGAGTG TTGTTCCAGT TTGGAACAAG AGTCCACTAT	2350
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GATGGCCAC TACGTGAACC ATCACCCTAA TCAAGTTTTT TGGGGTCGAG	2450
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GGGCGATCGG	TGCGGGCCTC	TTCGCTATTA	CGCCAGCTGG	CGAAAGGGGG	2800
ATGTGCTGCA	AGGCGATTAA	GTTGGGTAAC	GCCAGGGTTT	TCCCAGTCAC	2850
GACGTTGTAA	AACGACGGCC	AGTGCCAAGC	TAAAGGTGCA	CGGCCCCACGT	2900
GGCCACTAGT	ACTTCTCGAG	CTCTGTACAT	GTCCGCGGTC	GCGACGTACG	2950
CGTATCGATG	GCGCCAGCTG	CAGGCGGCCG	CCATATGCAT	CCTAGGCCCTA	3000
TTAATATTCC	GGAGTATACG	TAGCCGGCTA	ACGTTAACAA	CCGGTACCTC	3050
TAGAACTATA	GCTAGCCAAT	TCCATCATCA	ATAATATACC	TTATTTTGGGA	3100
TTGAAGCCAA	TATGATAATG	AGGGGGTGGA	GTTTGTGACG	TGGCGCGGGG	3150
CGTGGGAACG	GGGCGGGTGA	CGTAGGTTTT	AGGGCGGAGT	AACTTGTATG	3200
TGTTGGGAAT	TGTAGTTTTC	TTAAATGGG	AAGTTACGTA	ACGTGGGAAA	3250
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CAAATTTTCA	AAATAAAGCA	TTTTTTTTCAC	TGCATTCTAG	TTGTGGTTTG	3850
TCCAAACTCA	TCAATGTATC	TTATCATGTC	TGGATCCCCC	TAGCTTGCCA	3900
AACCTACAGG	TGGGGTCTTT	CATTCCCCCC	TTTTTCTGGA	GACTAAATAA	3950
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76

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TCTCCTCTTT	CAGAGCAGCA	ATCTGGGGCT	TAJACTTGCA	CTTGCTTGAG	4200
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GCTCCAATCA	CAATTAATAA	CAACTGGATG	AAGTCAAATA	TGGTAAGAGG	5600
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CACCTGCTTT	CAACGTGTTG	AGGGTTGACA	TAGGTGCTTG	AAGAACAGAA	5700
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GCGATCCACA	CGAAATGTGC	CAATGCAAGT	CCTTCATCAA	ATTTGTTTCAG	8000
GTTGTTGGAA	AGGAGACTAA	CAAGTTGTCC	AATACTTATT	TTATCTAGAA	8050
CACGGCTTGA	CAGCTTTAAA	GTCTTCTTAT	AAATCAAAC	AAACATAGCT	8100
ATTCTCATCT	GCATTCCAAT	GTGATGAAGG	CCAAAAATGG	CTGGGTGTAG	8150
GAGCAGTGTC	CTCACAATAA	AGAGAAGGCA	TAAGCCTATG	CCTAGATAAA	8200
TCGCGATAGA	GCGTTCCTCC	TTGTTATCCG	GGTCATAGGA	AGCTATGATT	8250
CTTCCCAGTA	AGAGAGGCTG	TACTGCTTTG	GTGACTTCCC	CTAAATATAA	8300
AAAGATTCCA	TAGAACATAA	ATCTCCAGAA	AAAACATCGC	CGAAGGGCAT	8350
TAATGAGTTT	AGGATTTTTT	TTTGAAGCCA	GCTCTCTATC	CCATTCTCTT	8400
TCCAATTTTT	CAGATAGATT	GTCAGCAGAA	TCAACAGAAG	GGATTTGGTA	8450
TATGTCTGAC	AATTCCAGGC	GCTGTCTGTA	TCCTTTCCTC	AAAATTGGTC	8500
TGGTCCAGCT	GAAAAAAAGT	TTGGAGACAA	CGCTGGCCTT	TTCCAGAGGC	8550
GACCTCTGCA	TGGTCTCTCG	GGCGCTGGGG	TCCCTGCTAG	GGCCGTCTGG	8600
GCTCAAGCTC	CTAATGCCAA	AGGAATTCCT	GCAGCCCGGG	GGATCCACTA	8650
GTTCTAGAGC	GGCCGCCACC	GCGGTGGCTG	ATCCCGCTCC	CGCCCGCCGC	8700
GCGCTTCGCT	TTTTATAGGG	CCGCCGCCGC	CGCCGCCTCG	CCATAAAAGG	8750
AACTTTTCGG	AGCGCGCCGC	TCTGATTGGC	TGCCGCCGCA	CCTCTCCGCC	8800
TCGCCCCGCC	CCGCCCCCTG	CCCCGCCCGC	CCCCGCCTGG	CGCGCGCCCC	8850
CCCCCCCCCC	CCGCCCCCAT	CGCTGCACAA	AATAATTAAA	AAATAAATAA	8900
ATACAAAATT	GGGGGTGGGG	AGGGGGGGGA	GATGGGGAGA	GTGAAGCAGA	8950
ACGTGGCCTC	GAGTAGATGT	ACTGCCAAGT	AGGAAAGTCC	CATAAGGTCA	9000
TGTACTGGGC	ATAATGCCAG	GCGGGCCATT	TACCGTCATT	GACGTCAATA	9050
GGGGGCGTAC	TTGGCATATG	ATACACTTGA	TGTACTGCCA	AGTGGGCAGT	9100
TTACCGTAAA	TACTCCACCC	ATTGACGTCA	ATGGAAAGTC	CCTATTGGCC	9150
TTACTATGGG	AACATACGTC	ATTATTGACG	TCAATGGGCG	GGGGTCGTTG	9200

80

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GGCGGTCAGC CAGGCGGGCC ATTTACCGTA AGTTATGTAA CGACCTGCAG 9250
GCTGATCTCC CTAGACAAAT ATTACGCGCT ATGAGTAACA CAAAATTATT 9300
CAGATTTTAC TTCCTCTTAT TCAGTTTTCC CGCGAAAATG GCCAAATCTT 9350
ACTCGGTTAC GCCCAAATTT ACTACAACAT CCJCTAAAA CCGCGCGAAA 9400
ATTGTCACCT CCTGTGTACA CCGGCGCACA CAAAAACGT CACTTTTGCC 9450
ACATCCGTCG CTTACATGTG TTCCGCCACA CTTGCAACAT CACACTTCCG 9500
CCACACTACT ACGTCACCCG CCCCCTTCCC ACGCCCCGCG CCACGTCACA 9550
AACTCCACCC CCTCATTATC ATATTGGCTT CAATCCAAAA TAAGGTATAT 9600
TATTGATGAT GCTAGCATGC GCAAATTTAA AGCGCTGATA TCGATCGCGC 9650
GCAGATCTGT CATGATGATC ATTGCAATTG GATCCATATA TAGGGCCCGG 9700
GTTATAATTA CCTCAGGTCG ACGTCCCATG GCCATTGCGA TTCGTAATCA 9750
TGGTCATAGC TGTTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA 9800
CAACATACGA GCCGGAAGCA TAAAGTGTA AGCCTGGGGT GCCTAATGAG 9850
TGAGCTAACT CACATTAATT GCGTTGCGCT CACTGCCCCG TTTCCAGTCG 9900
GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG 9950
AGGCGGTTTG CGTATTGGGC GC 9972

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAGTAAATTT GGGC

14

81

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGTAAGATTT GGCC

14

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTGAAATCT GAAT

14

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATAATTTT GTGT

14

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

82

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGTAATATTT GTCT

14

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

WANWTTTG

8

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19307 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAATTCCAT CATCAATAAT ATACCTTATT TTGGATTGAA GCCAATATGA	50
TAATGAGGGG GTGGAGTTTG TGACGTGGCG CGGGGCGTGG GAACGGGGCG	100
GGTGACGTAG GTTTTAGGGC GGAGTAACTT GTATGTGTTG GGAATTGTAG	150
TTTTCTTAAA ATGGGAAGTT ACGTAACGTG GGAAAACGGA AGTGACGATT	200
TGAGGAAGTT GTGGGTTTTT TGGCTTTCGT TTCTGGGCGT AGGTTTCGCGT	250
GCGGTTTTCT GGGTGTTTTT TGTGGACTTT AACCGTTACG TCATTTTTTA	300
GTCCTATATA TACTCGCTCT GCACTTGGCC CTTTTTTACA CTGTGACTGA	350
TTGAGCTGGT GCCGTGTCGA GTGGTGTTTT TTTAATAGGT TTTCTTTTTT	400

ACTGGTAAGG	CTGACTGTTA	GGCTGCCGCT	GTGAAGCGCT	GTATGTTGTT	450
CTGGAGCGGG	AGGGTGCTAT	TTTGCCTAGG	CAGGAGGGTT	TTTCAGGTGT	500
TTATGTGTTT	TTCTCTCCTA	TTAATTTTGT	TATACCTCCT	ATGGGGGCTG	550
TAATGTTGTC	TCTACGCCTG	CGGGTATGTA	T.CCCCCCAA	GCTTGCATGC	600
CTGCAGGTCG	ACTCTAGAGG	ATCCGAAAAA	ACCTCCCACA	CCTCCCCCTG	650
AACCTGAAAC	ATAAAATGAA	TGCAATTGTT	GTTGTTAACT	TGTTTATTGC	700
AGCTTATAAT	GGTTACAAAT	AAAGCAATAG	CATCACAAAT	TTCACAAATA	750
AAGCATTTTT	TTCACTGCAT	TCTAGTTGTG	GTTTGTCCAA	ACTCATCAAT	800
GTATCTTATC	ATGTCTGGAT	CCCCGCGGCC	GCTCTAGAAC	TAGTGGATCC	850
CCCCGGGCTG	AGGAATTCCG	TAACATAACT	GCGTGCTTTA	TTGAGATACA	900
CAGTAAAGCA	GTAATATAAT	ACAATAGTAA	GGCATATATT	TGGTGAAATC	950
TGATATGTTG	TGAAAATGCA	GTAAACTGA	AGTTTAAAAA	AATAATTAGT	1000
AAATGTTACA	GTGTTGGTGT	TAAACACAA	TCTATTATGA	TACTCAAGTA	1050
AGAGTCCAGT	ACCTGGAGAC	AATGATGATA	CATGCCATGT	GATGATTATG	1100
CTTCAGTTAC	ACTGATTATG	ATTTACACTT	TAATACTTGA	TGGTTATAAA	1150
GAACATGAAA	TGATGTCCAA	ATTATGCTTA	AAATCAGCAA	TAAAGCTCTC	1200
AGTTTTTATT	CAAATATTTT	GATAGATTCA	CTCCAGAACT	AATATCTAAA	1250
AGATAAACG	AAAAGATTAA	AACAAAATA	TGCACTCTAT	CTACCTTGGA	1300
TTTTAGAATG	AAACTTAAAA	CTTCTTAGTA	GGAAAGGAAC	CCCTTGTTTT	1350
AAATCTTGGT	GAAAACAAAT	CCTTGGATAA	AGAAAATGCC	CAGTGCCACA	1400
TAAAGGAGAG	AGAGAGAGAA	AAGCAAGACC	AGAACCAAAT	TTCAATTTGT	1450
TATCTTAGAG	CTTTGGGTTT	TCTTTTGGA	ATTATAAATG	AAAAAAGGAA	1500
ACTGGTGTCC	ACACAACAGA	CAAGTGGTGA	AGTTGTGAAA	TTAGGTGTGC	1550
ACAATTACTA	GAAACACCCC	AAAACCAAAG	TGAGGTAGAA	ATAGCATGAG	1600
AAGCTGTGTT	TGATGTTAAT	TACAATTAAT	AATGGACAAA	ACCCACTCGC	1650
TAGAAGTTAA	TTACACTTGA	CGTTAGAGGT	AACAGATTTG	CAAAATGATA	1700

84

GGACAGTGAT	TTCTATTGAG	AGAATGCTCT	TTAAATGCTA	AGAAGAAGAA	1750
ACTGGCATGA	GAGGAGTAAA	GCTCTTCCTA	GCAGTCCTTA	GCTTTCTGTT	1800
GCACTTTTTT	TCCTGGTTCA	ATGACTTGCA	TTTGTTTAGA	CATTTTCAGCC	1850
CGTCAACTAG	ACCAGAGAGT	TTGGAGACGC	TTTGCTCTC	AAAACCTTCC	1900
AACCACTGTG	CCTTCTCACC	CACAATCCTG	TGTGGAGTTA	CTTGCAGGGA	1950
AACCAATGCA	AAGGAGACAA	ATGCAGTTCA	TGGGCTTCTG	GA CTGATATT	2000
CACCAGGGTC	ACAATGTGAT	TGGGTTACTT	TCTTAACAGT	AATCCTAAGT	2050
CTTGCAGCAT	TA AAAAAAAA	AATCATCACA	ATGAAGAAAA	AAAAACCCAA	2100
AAAATCTAAA	ATCTAAAATT	CATCATCATC	ATCAACAACA	ACAACAACAA	2150
CAACAACAAA	ACCACCCACT	TCAGGTTGAG	TTTATGAAGA	GGGCAGAACA	2200
ATTTAGTTGT	AATTATAGAG	ATGTTTATAT	GTATAGTTGT	AAATATTCAT	2250
CCATTCTTTT	ACAGAGTTGT	TGCTCCCCTC	ATATAAATTG	ACTGAGGAGC	2300
CGCAACCTTT	AGCTCCTACC	ATCTTCCTCC	TACTGTCTGG	GAGTTAAAAA	2350
TGTCATCTGA	TGTTCTATTG	CAGAAACATC	ATTAAATATA	ACCCAACAGT	2400
AGGAAGTTGA	ATATATCAGC	CAACAAATTA	CTATGATAGT	AAGTCCTGTG	2450
TATTCATTCTG	CATGTTCTTT	GAAAAAAATG	AATCCTCTAG	CTCTCAGTGG	2500
AAAGTTTAAA	ACTAGAAACA	TCTGGAGCCC	TAGACAATAT	TTTAGTGTGG	2550
CGGTAGTCTC	CTGGCTTTGG	GCTCCAGGGA	AAATTCACTC	TTGCCCAAGC	2600
AGATAAGCCC	AGATGACTAG	AAGCAATTTC	CATTAGGAAG	TGGCAAGAAC	2650
ATTTGAAGAA	GTAACCTTCAT	ATCTATTTAT	CTATATACCT	ATAGTATTTA	2700
TATACTTGTA	GACATATAGA	TGTATAAAAT	GAAAGCCCAT	AGCCAGCCCC	2750
ACTCAGTCAA	CAATTCTCAA	AAGAGCAATA	TGAAGCAGTC	ATTTGGTGGG	2800
GTTCGTATGC	AAGAAAATAA	AAAAACGTCA	TGAATTCCAT	ATGAATACCA	2850
CGCTAAAGTA	ATGCAAAACA	ATGTGCTGCC	TCAGTGTGTG	TGTGTGTGTG	2900
TGTGTGTGTG	GTGGGTTCGT	GCATGTATGT	GTGCGTGTGT	GTGTGTGTGT	2950
GTGTGTGTGT	GTGTGTGTGC	GTGTGTGTTT	GTTTAGGGGT	TTTTATAAAC	3000

AACTTTTTTT	ATAAAGCAC	CTTTAGTTTA	CAATCTCTCT	TTATAACTGT	3050
TATAAATTTT	TAAACAACCC	AAAATGCGTT	CCATATAAAG	AAATGGCAAG	3100
TTATTTAGCT	ATCAAGATTT	TACATGTTTT	CTTTTAACTT	TTTGTACAA	3150
TTGCATAGAC	GTGTAAAACC	TGCCATTGTT	AAJAAAACAA	TAACAGACTT	3200
AGAAACTACT	GAAATCTACA	GTATAGTACC	ACTACCCTTC	ACAAAAATAT	3250
AGATTTTATT	TCTTGTAAC	TCTTACTGTC	TAATCCTCTT	TGTTGTACGA	3300
ATATTATAAA	AACCATGCGG	GAATCAGGAG	TTGTAAAACA	TTTATTCTGC	3350
TCCTTCTTCA	TCTGTCATGA	CTGAACTAA	GGACTCCATC	GCTCTGCCCA	3400
AATCATCTGC	CATGTGGAAA	AGGCTTCCTA	CATTGTGTCC	TCTCTCATTG	3450
GCTTTCGGG	GGCATTTCCT	CCTCTTGAAC	TAGGGAAGGA	GTTGTTGAGT	3500
TGCTCCATCA	CTTCTTCTAA	CCCTGTGCTT	GTGTCCTGGG	GAGGACTCAG	3550
AAGATCTTCC	TCACCCATAG	ATTCTGAAGT	TTGACTGCCA	ACCACTCGGA	3600
GCAGCATAGG	CTGACTGCTA	TCTGACCTCT	GCAGAGAGGT	GGAAGGAGAG	3650
GACACCGTGG	TGCCATTAC	CTTAGCTTCA	GCCTGGGGCT	GCTCCAGGAG	3700
CTGTCTCAGT	CTATGTAAC	GAGACTCCAG	CTGTTTATTG	TGGTCTTCCA	3750
GGATTTGCAT	CCTGGCTTCC	AGGCGTCCTT	TGTGTTGGCG	CAGTAGCTTA	3800
GCCTCAGCAA	TGAGCTCAGC	ATCCCTGGGA	CTCTGAGGAG	AGGTGGGCAT	3850
CATCTCAGGA	GGAGATGGCA	GTGGAGACAG	GCCTTTATGC	TCATGCTGCT	3900
GCTTCAGGCG	ATCATATTCT	GCTTGCAGAT	TCCTGTTTTT	TTCCTCAAGA	3950
TCTGCTAGGA	TTCTCTCTAG	CTCCCTCTT	TCCTCACTCT	CTAAGGAAAT	4000
CAAGATCTGG	GCAGGACTAC	GAGGCTGGCT	CAGGGGGGAG	TCCTGGTTCA	4050
AACTTTGGCA	GTAATGCTGG	ATTAACAAAT	GTTTCATCATC	TATGCTCTCA	4100
TTAGGAGAGA	TGCTATCATT	TAGATAAGAT	CCATTGCTGT	TTTCCATTTC	4150
TGCTAGCCTG	CTAGCATAAT	GTTCAATGCG	TGAATGAGTA	TCATCGTGTG	4200
AAAGCTGGGG	GGACGAGGCA	GGCGAGAAT	CTACTGGCCA	GAAGTTGATC	4250
AGAGTAACGG	GAGTTTCCAT	GTTGTCCCCC	TCTAACACAG	TCTGCACTGG	4300

86

CAGGTAGCCC	ATTCTGGGGAT	GCTTCGCAAA	ATACCTTTTG	GTTCGAAATT	4350
TGTTTTTTAG	TACCTTGGCG	AAGTCGCGAA	CATCTTCTCC	GGATGTAGTC	4400
GGAGTGCAAT	ACTCTACCAT	GGGGTAGTGC	ATTTTATGGC	CCTTTGCAAC	4450
TCGGCCAGAA	AAAAAGCAAC	TTTGGCAGAT	GTATAATTA	AAATGCTTTA	4500
GGCTTCTGTA	CCTGAATCCA	ATGATTGGAC	ACTCCTTACA	GATGTTACAC	4550
TTGGCTTGAT	GCTTGGCAGT	TTCAGCAGCA	GCCACTCTGT	GCAAGACGGG	4600
CAGCCACACC	ATAGACTGGG	GTTCCAGGCG	CATCCAGTCA	AGGAAGAGAG	4650
CAGCTTCAAT	CTCAGGTTTA	TTATTGGCAA	ATTGGAAGCA	GCTCCTGACA	4700
CTCGGCTCAA	TGTTACTGCC	CCCAAAGGAA	GCAACTTCAC	CCAACTGTCT	4750
TGGGATTTGA	ATAGAATCAT	GCAGAAGAAG	ACCCAGCCTA	CGCTGGTCAC	4800
AAAAGCCAGT	TGAAGTTGCC	ACTTGCTTGA	AAAGGTATCT	GTACTTGTCT	4850
TCCAAGTGTG	CTTTACACAG	AGAAATGATG	CCAGTTTTAA	AAGACAGGAC	4900
ACGGATCCTC	CCTGTTCGTC	CCGTATCATA	AACATTGAGA	AGCCAGTTGA	4950
GACACATATC	CACACAGAGA	GGGACATTGA	CCAGATTGTT	GTGCTCTTGC	5000
TCCAGACGAT	CATAAATTGT	AGTCAAACAG	TTAATTATCT	GCAGGATATC	5050
CATGGGCTGG	TCATTTTGCT	TGAGGTTGTG	CTGGTCCAGG	GCATCACATG	5100
CAGCTGACAG	GCTCAAGAGA	TCCAAGCAAA	GGGCCTTCTG	GAGCCTTCTG	5150
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TAAAGACTGG	TAGAGCTCTG	TCATTTTGGG	GTGGTCCCAA	CAAGTGGTTT	5250
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TCCCAGGGAC	CCTGAAGTGA	AGTGAAAGG	AAGTGCTGGG	ATGCAGGACC	5350
AAAGTCCCTG	TGGGCTTCAT	GCAGCTGTCT	GACACGGTCC	TCCACAGCCA	5400
CCTGTAGAAG	CCTCCATCTG	GTATTCAGAT	CTTCCAAAGT	GCTGAGGTTA	5450
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GACACGATTG	ACATTCTCTT	TAAGAGGTGC	AATTCTCTCC	CGAAGTGCCT	5550
TGACTTTTTTC	AAGGTGATCT	TGCAGAGAGT	CAATGAGGAG	ATCCCCCACT	5600

GGCTGCCAGG	ATCCCTTGAT	CACCTCAGCT	TGGCGCAACT	TGAGGTCCAG	5650
TTCATCGGCA	GCTTCCTGAA	GTTCTGGAG	TCTTTCAAGA	GCTTCATCTA	5700
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TTGACCTCTT	CAGCCTGCTT	TCGTAGGAGC	CLAGTGACAT	TCTGAGCTCT	5800
TTCTTCAGGA	GGCAGTTCTC	TGGGCTCCTG	GTAGAGTTTC	TCTAGTCCTT	5850
CCAAAGGCTG	CTCTGTCAGA	AATATTCTCA	CAGTCTCCAG	AGTACTCATG	5900
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TCAGTTCATC	ATCTTTCAGC	TGTAGCCAAA	CAAGAAGTTC	CTGAAGAGAA	6050
AGATGCAAAC	GCTTCCACTG	GTCAGAACTT	GCTTCCAAAT	GGGACCTAAT	6100
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AACGTCTTTG	TAACAGGGGT	GCTTCATCCG	AACCTTCCAG	GGATCTCAGG	6200
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AATTTCTCCT	TGGAGATCTT	GCCATGGTTT	CATCAGCTCT	CTGACTCCCC	6300
TGGAGTCTTC	TAGGAGCTTC	TCCTTACGGG	AAGCGTCCTG	TAGGACATTG	6350
GCAGTTGTTT	CTGCTTCCGT	AATCCAGGAA	AGAACTTCT	CCAGGTCCAG	6400
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CACTTACTCT	TTTATGAATG	TTCCCCAAG	AAGTATTGAT	ATTCTCTGTT	6500
ATCATGTGTA	CTTTTCTGGT	ATCATCAGCA	GAATAGTCCC	GAAGAAGTTT	6550
CAGTGCCAAA	TCATTTGCCA	CGTCTACACT	TATCTGCCGT	TGACGGAGGT	6600
CTTTGGCCAA	CTGCTTGGTT	TCTGTGATCT	TCTTTTGGAT	TGCATCTACT	6650
GTGTGAGGAC	CTTCTTTCCA	TGAGTCAAGC	TTGCCTCTGA	CCTGTCCTAT	6700
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TTCTTGATTG	CTGGTTTTGT	TTTTCAAATT	CTGGGCAGCA	GTAATGAGTT	6900

88

CTTCCAATTG	GGGGCGTCTC	TGTTCCAAAT	CTTGCAAGTG	TGCCTTCTGT	6950
TTGATGATCA	TTTCATTGAT	GTCTTCCAGA	TCACCCACCA	TCACTCTCTG	7000
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CACTAGAGTA	ACAGTCTGAC	TGGCAGAGGC	TCCAGTAGTG	CTCAGTCCAG	7200
GGGCACGGTC	AGGCTGCTTT	GTCCTCAGCT	CCCGAAGTAA	ATGGTTTACA	7250
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GCTTGGTTTT	TCCTTATACA	AATGCTGCCC	TTTCGACAAA	AGCCTTTCCA	7350
CATCCGCTTG	TTTACCGTGA	ACTGTTACTT	CAATCTCCTT	TATGTCAAAC	7400
GGTCCTGCCT	GACTTGCTTG	GTTATAAATT	TCCAACGGT	TTCTAATAGG	7450
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ACCTTTATCC	ACTGGAGATT	TGTCTGTTTG	AGCTTCTTTT	CAAGTTTATC	7600
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CCAATGCCAT	CCTGGAGTTC	CTTAAGATAC	CATTGTATT	TAGCATGTTT	8050
CCAGTTTTC	GGATTTTGTG	TCTTTTGA	AACTGTTCA	ACTTCATTCA	8100
GCCATTGATT	AAATACCTTC	ATATCATAAT	GAAAGTGTCG	CCATTTTTC	8150
ACTGATCTGT	CGAATCGCCC	TTGTCGTTCC	TTGTACATTC	TATGAAGTTT	8200

TTCCCCCTGG	AAATCCATCT	GTGCCACGGC	TTCCTGTACT	TTCACCTTTT	8250
CCATGGAGGT	GGCACTTTGC	AAGGCTGCTG	TCTTCTTCTT	GTGAATAATA	8300
TCAATCCGAC	CTGAGATTTG	TTGCAAATTG	TCTTTTATAT	TCTTAAGAGA	8350
CTCCTCTTGC	TTAAAAAGAT	CTTCAAAATC	T.TAGCACAG	AGTTCAGGAG	8400
TATTTAGAAG	ATGATCAACT	TCTGAAAGAG	CTTGTAAGAT	ATGACTGATC	8450
TGGTCAAAT	AAGTAGAAGG	CACATAAGAA	ACATCCAAAG	GCATATCTTC	8500
AGTCGTCACT	ACCATAGTTT	CTTCATGGAG	AGTGTGAATT	TGTGCAAAGT	8550
TGAGTCTTCG	AAACTGAGCA	AAATTGCTCT	CAATTTGCCG	CCAGCGCTTG	8600
CTGAGCTGGA	TCTGAGTTGG	CTCCACTGCC	ATTGCGGCCC	CATTCTCAGA	8650
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GCAATTCACG	ATCAATTTCC	TTTAATTTTC	TTTCATCTCT	GGGTTCAGGT	8750
AGGCTGGCTA	ATTTTTTTTC	AATTTTCATCC	AAGCATTTCA	GGAGATCATC	8800
AGCCTGCCTC	TTGTACTGAT	ACCACTGGTG	AGAAATTTCT	AGGGCCTTTT	8850
TTCTTCTTTG	AGACCTCAAA	TCCTTGAGAG	CATTATGTTT	TGTCTGTAAC	8900
AGCTGCTGTT	TTATCTTTAT	TTCTCTCGC	TTTCTCTCAT	CTGTGATTCT	8950
TTGTTGTAAG	TTGTCTCCTC	TTTGCAACAA	TTCATTTACA	GTACCCTCAT	9000
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TGCTGAATTT	CAGCCTCCAG	TGGTTCAAGC	AATTTTTGTA	TATCTGAGTT	9100
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TGTGAGAAAT	AGCTGCAAAT	CGACGGTTGA	GCTCAGAGAT	TTGGGGCTCT	9200
ACTACTTTCC	TGCAGTGGTC	ACCGCGGTTT	GCCATCAATT	TTGCTGCTTG	9250
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AACGCTTAAG	AATGTCTTCC	TTTTGTGTGT	GTTTCTTCTT	TTCAGACTCA	9350
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CCGGGCC 19307

WHAT IS CLAIMED IS:

1. A recombinant shuttle vector comprising:
 - (a) the DNA sequences of, or corresponding to, a portion of the genome of an adenovirus which comprises DNA sequences of, or corresponding to, the adenovirus 5' and 3' inverted terminal repeats and packaging/enhancer domain necessary for replication and virion encapsidation in the absence of sequence encoding viral genes;
 - (b) a selected gene operatively linked to regulatory sequences directing its expression, said gene operatively linked to the DNA of (a) and capable of expression in a target cell *in vivo* or *in vitro*.
2. The vector according to claim 1 wherein said DNA sequences (a) comprise the native adenovirus 5' inverted terminal repeats and packaging sequences.
3. The vector according to claim 1 wherein said DNA sequences (a) comprise the native adenovirus 3' inverted terminal repeat sequences.
4. The vector according to claim 1 wherein said selected gene (b) is a reporter gene.
5. The vector according to claim 4 wherein said reporter gene is selected from the group consisting of the genes encoding β -galactosidase, alkaline phosphatase and green fluorescent protein.
6. The vector according to claim 1 wherein said selected gene (b) is a therapeutic gene.

7. The vector according to claim 6 wherein said therapeutic gene is selected from the group consisting of a normal CFTR gene, a DMD Becker allele and a normal LDL gene.

8. A crippled adenovirus helper virus comprising a modified adenovirus sequence in place of native adenovirus sequence map units 0-1, which modification reduces the packaging efficiency of said virus, said virus also containing selected adenovirus genes necessary to direct a productive viral infection.

9. The helper virus according to claim 8 wherein said modified sequence comprises:

- i. a fragment of adenovirus map units 0-1;
- ii. a fragment of (i) containing a 5' inverted terminal repeat and between one to four selected packaging sequences,
- iii. a modified fragment of (i) containing at least one PAC consensus sequence in place of at least one native PAC sequence; and
- iv. a modified fragment of (ii), wherein said native PAC sequences are mutated to contain modified sequences.

10. The virus according to claim 8 wherein said modified sequence comprises Ad5 base pairs 1-269.

11. The virus according to claim 8 wherein said sequence (ii) comprises Ad5 base pairs 1-321.

12. The virus according to claim 8 wherein said helper adenovirus is conjugated to a poly-cation sequence.

13. A method for producing a recombinant adenovirus which comprises transfecting a selected host cell with

- (a) a recombinant shuttle vector comprising
 - i. the DNA sequences of, or corresponding to, a portion of the genome of an adenovirus which comprises adenovirus 5' and 3' cis-elements necessary for replication and virion encapsidation in the absence of sequence encoding viral genes; and
 - ii. a selected gene operatively linked to regulatory sequences directing its expression, said gene linked to the DNA of (a) and capable of expression in a target cell *in vivo* or *in vitro*; and

- (b) a helper adenovirus comprising sufficient adenovirus gene sequences necessary for a productive viral infection, wherein said transfected host cell permits the formation of a recombinant virus comprising the DNA of (i) and (ii) in an adenoviral capsid, and isolating and purifying the recombinant virus from said cell.

14. The method according to claim 13, wherein said helper virus is a crippled helper virus comprising a modified adenovirus sequence in place of native adenovirus sequence map units 0-1, which modification reduces the packaging efficiency of said helper virus, said helper virus also containing selected adenovirus genes necessary to direct a productive viral infection.

15. The method according to claim 13 wherein said helper adenovirus is associated with a poly-cation sequence.

16. The method according to claim 13 wherein said vector is associated with said helper adenovirus conjugate in a single particle.

17. The method according to claim 13 wherein said helper virus is an adenovirus sequence containing deletions of all or portions of the E1a and E1b genes.

18. The method according to claim 13 wherein said helper virus is an adenovirus sequence containing deletions of all or a portion of the E3 gene.

19. A recombinant adenovirus comprising

i. the DNA of, or corresponding to, a portion of the genome of an adenovirus which comprises adenovirus 5' and 3' cis-elements necessary for replication and virion encapsidation in the absence of sequence encoding viral genes;

ii. a selected gene operatively linked to regulatory sequences directing its expression, said gene linked to the DNA of (a) and capable of expression in a target cell *in vivo* or *in vitro*;

said DNA and gene encapsidated in an adenoviral capsid.

20. The virus according to claim 19 wherein said viral capsid is a capsid of an adenovirus serotype selected from the group consisting of types 2, 4, 5, 7, 12 and 40.

21. The virus according to claim 19 wherein said selected gene is a CFTR gene, a DMD gene and an LDL gene.

102

22. The use of a recombinant ad novirus according to claim 19 for the manufacture of a pharmaceutical composition suitable for delivering and integrating a selected gene into the chromosome of a target cell.

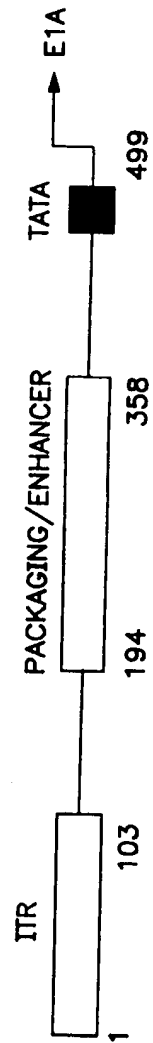


FIG. 1A

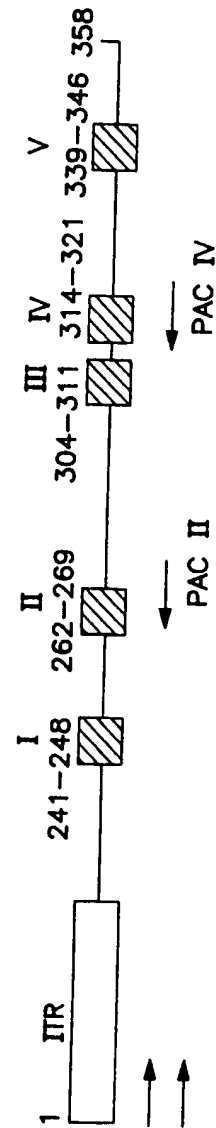
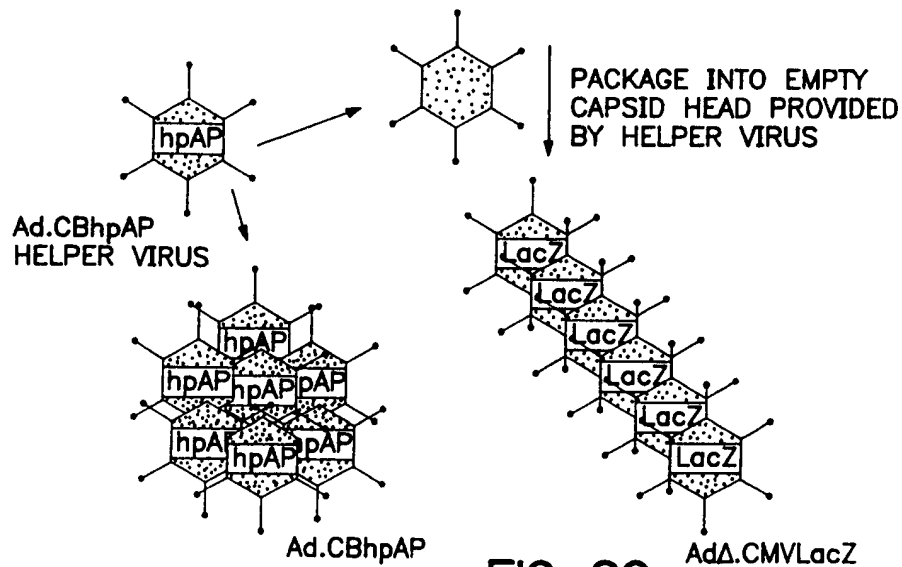
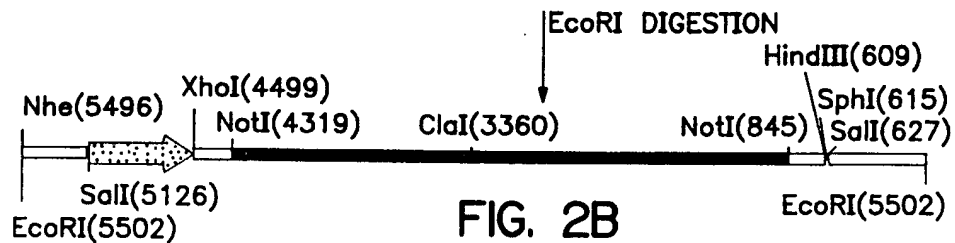
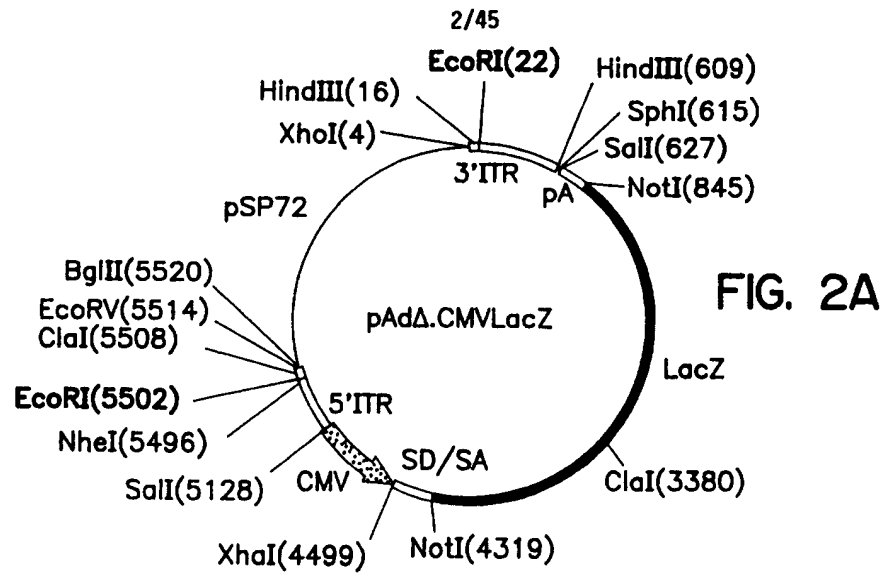


FIG. 1B



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FIGURE 3A

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TTCCCCCAA	GCTTGCAATG	CTGCAGGTCG	ACTCTAGAGG	ATCCGAAAAA	650
ACCTCCCACA	CCTCCCCCTG	AACCTGAAAC	ATAAAATGAA	TGCAATTGTT	700
GTTGTTAACT	TGTTTATTGC	AGCTTATAAT	GGTTACAAAT	AAAGCAATAG	750
CATCACAAAT	TTCACAAATA	AAGCATTTTT	TTCAGTGCAT	TCTAGTTGTG	800
GTTTGTCCAA	ACTCATCAAT	GTATCTTATC	ATGTCTGGAT	CCCCGCGGCC	850
GCCTAGAGTC	GAGGCCGAGT	TTGTCAGAAA	GCAGACCAA	CAGCGGTTGG	900
AATAATAGCG	AGAACAGAGA	AATAGCGGCA	AAAATAATAC	CCGTATCACT	950
TTTGCTGATA	TGGTTGATGT	CATGTAGCCA	AATCGGGAAA	AACGGGAAGT	1000
AGGCTCCCAT	GATAAAAAAG	TAAAAGAAAA	AGAATAAAAC	GAACATCCAA	1050
AAGTTTGTGT	TTTTTAAATA	GTACATAATG	GATTTCTTAA	CGCGAAATAC	1100
GGGCAGACAT	GGCCTGCCCC	GTTATTATTA	TTTTTGACAC	CAGACCAACT	1150
GGTAATGGTA	GCGACCGGCG	CTCAGCTGTA	ATTCCGCCGA	TACTGACGGG	1200
CTCCAGGAGT	CGTCGCCACC	AATCCCCATA	TGGAAACCGT	CGATATTTCAG	1250
CCATGTGCCT	TCTTCCGCGT	GCAGCAGATG	GCGATGGCTG	CTTTCCATCA	1300
GTTGCTGTTG	ACTGTAGCGG	CTGATGTTGA	ACTGGAAGTC	GCCGCGCCAC	1350

4/45

FIGURE 3B

TGGTGTGGGC	CATAATTCAA	TTCGCGCGTC	CCGCAGCGCA	GACCGTTTTTC	1400
GCTCGGGAAG	ACGTACGGGG	TATACATGTC	TGACAATGGC	AGATCCCAGC	1450
GGTCAAAACA	GGCGGCAGTA	AGGCGGTTCG	GATAGTTTTTC	TTGCGGCCCT	1500
AATCCGAGCC	AGTTTACCCG	CTCTGCTACC	TGCGCCAGCT	GGCAGTTCAG	1550
GCCAAATCCGC	GCCGGATGCG	GTGTATCGCT	CGCCACTTCA	ACATCAACGG	1600
TAATCGCCAT	TTGACCACTA	CCATCAATCC	GGTAGGTTTT	CCGGCTGATA	1650
AATAAGGTTT	TCCCCTGATG	CTGCCACGCG	TGAGCGGTCTG	TAATCAGCAC	1700
CGCATCAGCA	AGTGTATCTG	CCGTGCACTG	CAACAACGCT	GCTTCGGCCT	1750
GGTAATGGCC	CGCCGCCTTC	CAGCGTTCGA	CCCAGGCGTT	AGGGTCAATG	1800
CGGGTCGCTT	CACTTACGCC	AATGTCGTTA	TCCAGCGGTG	CACGGGTGAA	1850
CTGATCGCGC	AGCGGCGTCA	GCAGTTGTTT	TTTATCGCCA	ATCCACATCT	1900
GTGAAAGAAA	GCCTGACTGG	CGGTTAAATT	GCCAACGCTT	ATTACCCAGC	1950
TCGATGCAAA	AATCCATTTC	GCTGGTGGTC	AGATGCGGGA	TGGCGTGGGA	2000
CGCGGCGGGG	AGCGTCACAC	TGAGGTTTTTC	CGCCAGACGC	CACTGCTGCC	2050
AGGCGCTGAT	GTGCCCCGGT	TCTGACCATG	CGGTCGCGTT	CGGTTGCACT	2100
ACGCGTACTG	TGAGCCAGAG	TTGCCCCGGC	CTCTCCGGCT	GCGGTAGTTC	2150
AGGCAGTTCA	ATCAACTGTT	TACCTTGTGG	AGCGACATCC	AGAGGCACTT	2200
CACCGCTTGC	CAGCGGCTTA	CCATCCAGCG	CCACCATCCA	GTGCAGGAGC	2250
TCGTTATCGC	TATGACGGAA	CAGGTATTCG	CTGGTCACTT	CGATGGTTTTG	2300
CCCGGATAAA	CGGAACTGGA	AAAAGTCTG	CTGGTGTTTT	GCTTCCGTCA	2350
GCGCTGGATG	CGGCGTGCGG	TCGGCAAAGA	CCAGACCGTT	CATACAGAAC	2400
TGGCGATCGT	TCGGCGTATC	GCCAAAATCA	CCGCCGTAAG	CCGACCACGG	2450
GTTGCCGTTT	TCATCATATT	TAATCAGCGA	CTGATCCACC	CAGTCCCAGA	2500
CGAAGCCGCC	CTGTAAACGG	GGATACTGAC	GAAACGCCTG	CCAGTATTTA	2550
GCGAAACCGC	CAAGACTGTT	ACCCATCGCG	TGGGCGTATT	CGCAAAGGAT	2600
CAGCGGGCGC	GTCTCTCCAG	GTAGCGAAAG	CCATTTTTTG	ATGGACCATT	2650

SEQUENCE LISTING

FIGURE 3C

TCGGCACAGC	CGGGAAGGGC	TGGTCTTCAT	CCACGCGCGC	GTACATCGGG	2700
CAAATAATAT	CGGTGGCCGT	GGTGTGGGCT	CCGCCGCCTT	CATACTGCAC	2750
CGGGCGGGAA	GGATCGACAG	ATTTGATCCA	GCGATACAGC	GCGTCGTGAT	2800
TAGCGCCGTG	GCCTGATTCA	TTCCCCAGCG	ACCAGATGAT	CACACTCGGG	2850
TGATTACGAT	CGCGCTGCAC	CATTGCGGTT	ACGCGTTTCG	TCATCGCCGG	2900
TAGCCAGCGC	GGATCATCGG	TCAGACGATT	CATTGGCACC	ATGCCGTGGG	2950
TTTCAATATT	GGCTTCATCC	ACCACATACA	GGCCGTAGCG	GTGCGACAGC	3000
GTGTACCACA	GCGGATGGTT	CGGATAATGC	GAACAGCGCA	CGGCGTTAAA	3050
GTTGTTCTGC	TTCATCAGCA	GGATATCCTG	CACCATCGTC	TGCTCATCCA	3100
TGACCTGACC	ATGCAGAGGA	TGATGCTCGT	GACGGTTAAC	GCCTCGAATC	3150
AGCAACGGCT	TGCCGTTTCA	CAGCAGCAGA	CCATTTTCAA	TCCGCACCTC	3200
GCGGAAACCG	ACATCGCAGG	CTTCTGCTTC	AATCAGCGTG	CCGTCGGCGG	3250
TGTGCAGTTC	AACCACCGCA	CGATAGAGAT	TCGGGATTTT	GGCGCTCCAC	3300
AGTTTCGGGT	TTTCGACGTT	CAGACGTAGT	GTGACGCGAT	CGGCATAACC	3350
ACCACGCTCA	TCGATAATTT	CACCGCCGAA	AGGCGCGGTG	CCGCTGGCGA	3400
CCTGCGTTTC	ACCCTGCCAT	AAAGAACTG	TTACCCGTAG	GTAGTCACGC	3450
AACTCGCCGC	ACATCTGAAC	TTCAGCCTCC	AGTACAGCGC	GGCTGAAATC	3500
ATCATTAAAG	CGAGTGGCAA	CATGGAAATC	GCTGATTTGT	GTAGTCGGTT	3550
TATGCAGCAA	CGAGACGTCA	CGGAAAATGC	CGCTCATCCG	CCACATATCC	3600
TGATCTTCCA	GATAACTGCC	GTCACCTCAA	CGCAGCACCA	TCACCGCGAG	3650
GCGGTTTTCT	CCGGCGCGTA	AAAATGCGCT	CAGGTCAAAT	TCAGACGGCA	3700
AACGACTGTC	CTGGCCGTAA	CCGACCCAGC	GCCCGTTGCA	CCACAGATGA	3750
AACGCCGAGT	TAACGCCATC	AAAAATAATT	CGCGTCTGGC	CTTCCTGTAG	3800
CCAGCTTTCA	TCAACATTAA	ATGTGAGCGA	GTAACAACCC	GTCGGATTCT	3850
CCGTGGGAAC	AAACGGCGGA	TTGACCGTAA	TGGGATAGGT	TACGTTGGTG	3900
TAGATGGGCG	CATCGTAACC	GTGCATCTGC	CAGTTTGAGG	GGACGACGAC	3950

6/45

FIGURE 3D

AGTATCGGCC	TCAGGAAGAT	CGCACTCCAG	CCAGCTTTCC	GGCACCGCTT	4000
CTGGTGCCGG	AAACCAGGCA	AAGCGCCATT	CGCCATTTCAG	GCTGCGCAAC	4050
TGTTGGGAAG	GGCGATCGGT	GCGGGCCTCT	TCCTATTAC	GCCAGCTGGC	4100
CAAAGGGGGA	TGTGCTGCAA	GGCGATTAAAG	TTGGGTAACG	CCAGGGTTTT	4150
CCCAGTCACG	ACGTTGTAAA	ACGACGGGAT	CGCGCTTGAG	CAGCTCCTTG	4200
CTGGTGTCCA	GACCAATGCC	TCCCAGACCG	GCAACGAAAA	TCACGTTCTT	4250
GTTGGTCAAA	GTAAACGACA	TGGTGACTTC	TTTTTTGCTT	TAGCAGGCTC	4300
TTTCGATCCC	CGGGAATTGC	GGCCGCGGGT	ACAATTCCGC	AGCTTTTAGA	4350
GCAGAAGTAA	CAC TTCGTA	CAGGCCTAGA	AGTAAAGGCA	ACATCCACTG	4400
AGGAGCAGTT	CTTTGATTTG	CACCACCACC	GGATCCGGGA	CCTGAAATAA	4450
AAGACAAAAA	GACTAAACTT	ACCAGTTAAC	TTTCTGGTTT	TTCAGTTCCT	4500
CGAGTACCGG	ATCCTCTAGA	GTCCGGAGGC	TGGATCGGTC	CCGGTCTCTT	4550
CTATGGAGGT	CAAAACAGCG	TGGATGGCGT	CTCCAGGCGA	TCTGACGGTT	4600
CACTAAACGA	GCTCTGCTTA	TATAGACCTC	CCACCGTACA	CGCCTACCGC	4650
CCATTTGCGT	CAATGGGGCG	GAGTTGTTAC	GACATTTTGG	AAAGTCCCGT	4700
TGATTTTGGT	GCCAAAACAA	ACTCCCATTG	ACGTCAATGG	GGTGGAGACT	4750
TGGAAATCCC	CGTGAGTCAA	ACCGCTATCC	ACGCCCATTG	ATGTACTGCC	4800
AAAACCGCAT	CACCATGGTA	ATAGCGATGA	CTAATACGTA	GATGTACTGC	4850
CAAGTAGGAA	AGTCCCATAA	GGTCATGTAC	TGGGCATAAT	GCCAGGCGGG	4900
CCATTTACCG	TCATTGACGT	CAATAGGGGG	CGTACTTGGC	ATATGATACA	4950
CTTGATGTAC	TGCCAAGTGG	GCAGTTTACC	GTAAATACTC	CACCCATTGA	5000
CGTCAATGGA	AAGTCCCTAT	TGGCGTTACT	ATGGGAACAT	ACGTCATTAT	5050
TGACGTCAAT	GGGCGGGGGT	CGTTGGGCGG	TCAGCCAGGC	GGGCCATTTA	5100
CCGTAAGTTA	TGTAACGACC	TGCAGGTCGA	CTCTAGAGGA	TCTCCCTAGA	5150
CAAATATTAC	GCGCTATGAG	TAACACAAAA	TTATTCAGAT	TTCACTTCCT	5200
CTTATTCAGT	TTTCCCGCGA	AAATGGCCAA	ATCTTACTCG	GTTACGCCCA	5250

SUBSTITUTE SHEET (RULE 26)

FIGURE 3E

AATTTACTAC	AACATCCGCC	TAAAACCGCG	CGAAAATTGT	CACTTCCTGT	5300
GTACACCGGC	GCACACCAA	AACGTCACCT	TTGCCACATC	CGTCGCTTAC	5350
ATGTGTTCCG	CCACACTTGC	AACATCACAC	TTCCGCCACA	CTACTACGTC	5400
ACCCGCCCCG	TTCCCACGCC	CCGCGCCACG	TCACAAACTC	CACCCCCTCA	5450
TTATCATATT	GGCTTCAATC	CAAAATAAGG	TATATTATTG	ATGATGCTAG	5500
CGAATTCATC	GATGATATCA	GATCTGCCGG	TCTCCCTATA	GTGAGTCGTA	5550
TTAATTTTCA	TAAGCCAGGT	TAACCTGCAT	TAATGAATCG	GCCAACGCGC	5600
GGGGAGAGGC	GGTTTGCCTA	TTGGGCGCTC	TTCCGCTTCC	TCGCTCACTG	5650
ACTCGCTGCG	CTCGGTCGTT	CGGCTGCGGC	GAGCGGTATC	AGCTCACTCA	5700
AAGGCGGTAA	TACGGTTATC	CACAGAATCA	GGGGATAACG	CAGGAAAGAA	5750
CATGTGAGCA	AAAGGCCAGC	AAAAGGCCAG	GAACCGTAAA	AAGGCCGCGT	5800
TGCTGGCGTT	TTTCCATAGG	CTCCGCCCCC	CTGACGAGCA	TCACAAAAAT	5850
CGACGCTCAA	GTCAGAGGTG	GCGAAACCCG	ACAGGACTAT	AAAGATACCA	5900
GGCGTTTCCC	CCTGGAAGCT	CCCTCGTGCG	CTCTCCTGTT	CCGACCCTGC	5950
CGCTTACCGG	ATACCTGTCC	GCCTTTCTCC	CTTCGGGAAG	CGTGGCGCTT	6000
TCTCAATGCT	CACGCTGTAG	GTATCTCAGT	TCGGTGTAGG	TCGTTGCTC	6050
CAAGCTGGGC	TGTGTGCACG	AACCCCCCGT	TCAGCCCGAC	CGCTGCGCCT	6100
TATCCGGTAA	CTATCGTCTT	GAGTCCAACC	CGGTAAGACA	CGACTTATCG	6150
CCACTGGCAG	CAGCCACTGG	TAACAGGATT	AGCAGAGCGA	GGTATGTAGG	6200
CGGTGCTACA	GAGTTCTTGA	AGTGGTGGCC	TAACTACGGC	TACACTAGAA	6250
GGACAGTATT	TGGTATCTGC	GCTCTGCTGA	AGCCAGTTAC	CTTCGGAAAA	6300
AGAGTTGGTA	GCTCTTGATC	CGGCAAACAA	ACCACCGCTG	CTAGCGGTGG	6350
TTTTTTTTGTT	TGCAAGCAGC	AGATTACGCG	CAGAAAAAAA	GGATCTCAAG	6400
AAGATCCTTT	GATCTTTTCT	ACGGGGTCTG	ACGCTCAGTG	GAACGAAAAAC	6450
TCACGTTAAG	GGATTTTGGT	CATGAGATTA	TCAAAAAGGA	TCTTCACCTA	6500
GATCCTTTTA	AATTAAAAAT	GAAGTTTAA	ATCAATCTAA	AGTATATATG	6550

8/45

FIGURE 3F

AGTAAACTTG	GTCTGACAGT	TACCAATGCT	TAATCAGTGA	GGCACCTATC	6600
TCAGCGATCT	GTCTATTTTCG	TTCATCCATA	GTTGCCTGAC	TCCCCGTCGT	6650
GTAGATAACT	ACGATACGGG	AGGGCTTACC	ATCTGGCCCC	AGTGCTGCAA	6700
TGATACCGCG	AGACCCACGC	TCACCGGCTC	C/ GATTTATC	AGCAATAAAC	6750
CAGCCAGCCG	GAAGGGCCGA	GCGCAGAAGT	GGTCCTGCAA	CTTTATCCGC	6800
CTCCATCCAG	TCTATTAATT	GTTGCCGGGA	AGCTAGAGTA	AGTAGTTCGC	6850
CAGTTAATAG	TTTGCGCAAC	GTTGTTGCCA	TTGCTACAGG	CATCGTGGTG	6900
TCACGCTCGT	CGTTTGGTAT	GGCTTCATTC	AGTCCGGTT	CCCAACGATC	6950
AAGGCGAGTT	ACATGATCCC	CCATGTTGTG	CAAAAAGCG	GTTAGCTCCT	7000
TCGGTCCTCC	GATCGTTGTC	AGAAGTAAGT	TGGCCGCAGT	GTTATCACTC	7050
ATGGTTATGG	CAGCACTGCA	TAATTCTCTT	ACTGTCATGC	CATCCGTAAG	7100
ATGCTTTTCT	GTGACTGGTG	AGTACTCAAC	CAAGTCATTC	TGAGAATAGT	7150
GTATGCGGCG	ACCGAGTTGC	TCTTGCCCGG	CGTCAATACG	GGATAATACC	7200
GCGCCACATA	GCAGAACTTT	AAAAGTGCTC	ATCATTGGAA	AACGTTCTTC	7250
GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT	GTTGAGATCC	AGTTCGATGT	7300
AACCCACTCG	TGCACCCAAC	TGATCTTCAG	CATCTTTTAC	TTTCACCAGC	7350
GTTTCTGGGT	GAGCAAAAAC	AGGAAGGCAA	AATGCCGCAA	AAAAGGGAAT	7400
AAGGGCGACA	CGGAAATGTT	GAATACTCAT	ACTCTTCCTT	TTTCAATATT	7450
ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA	TGAGCGGATA	CATATTTGAA	7500
TGTATTTAGA	AAAATAAACA	AATAGGGGTT	CCGCGCACAT	TTCCCCGAAA	7550
AGTGCCACCT	GACGTCTAAG	AAACCATTAT	TATCATGACA	TTAACCTATA	7600
AAAATAGGCG	TATCACGAGG	CCCTTTCGTC	TCGCGCGTTT	CGGTGATGAC	7650
GGTGAAAACC	TCTGACACAT	GCAGCTCCCG	GAGACGGTCA	CAGCTTGTCT	7700
GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG	7750
TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG	CGGCATCAGA	GCAGATTGTA	7800
CTGAGAGTGC	ACCATATGGA	CATATTGTGC	TTAGAACGCG	GCTACAATTA	7850
ATACATAACC	TTATGTATCA	TACACATACG	ATTTAGGTGA	CACTATA	7897

SUBSTITUTE SHEET (RULE 96)

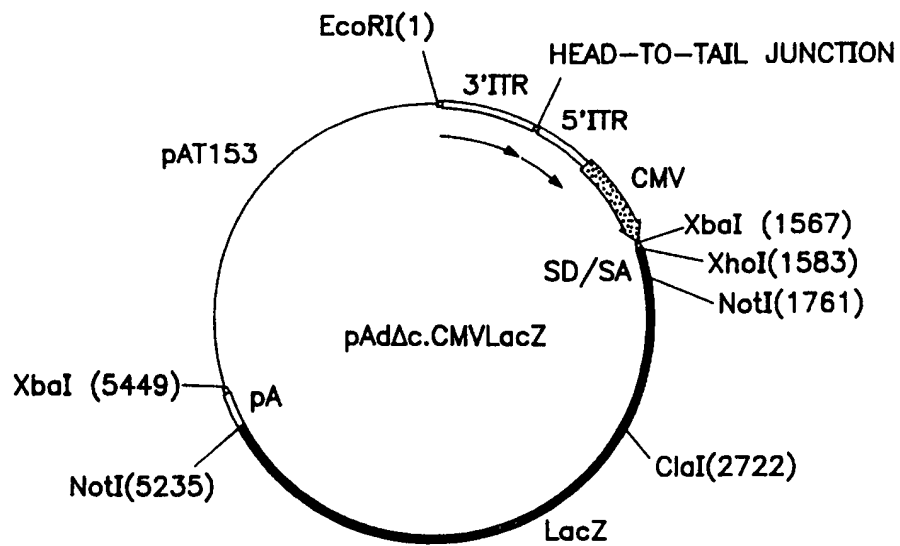


FIG. 4A

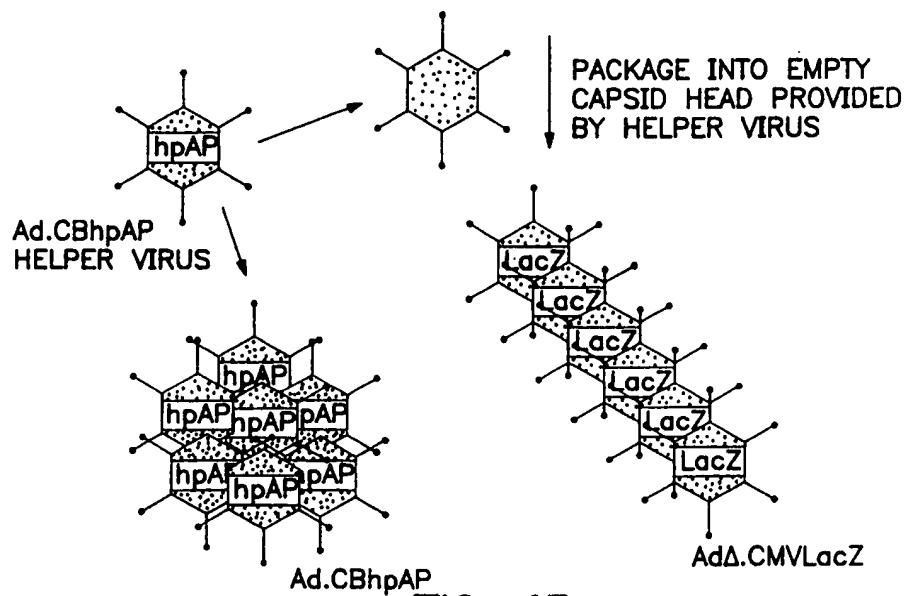


FIG. 4B

10/45

FIGURE 5A

GAATTCGCTA	GCTAGCGGGG	GAATACATAC	CCGCAGGCGT	AGAGACAACA	50
TTACAGCCCC	CATAGGAGGT	ATAACAAAAT	TAATAGGAGA	GAAAAACACA	100
TAAACACCTG	AAAAACCCTC	CTGCCTAGGC	AAAATAGCAC	CCTCCCGCTC	150
CAGAACAACA	TACAGCGCTT	CACAGCGGCA	GCCTAACAGT	CAGCCTTACC	200
AGTAAAAAAG	AAAACCTATT	AAAAAAACAC	CACTCGACAC	GGCACCAGCT	250
CAATCAGTCA	CAGTGTAATA	AAGGGCCAAG	TGCAGAGCGA	GTATATATAG	300
GACTAAAAAA	TGACGTAACG	GTAAAGTCC	ACAAAAACA	CCCAGAAAAC	350
CGCACGCGAA	CCTACGCCCC	GAAACGAAAG	CCAAAAAACC	CACAACTTCC	400
TCAAATCGTC	ACTTCCGTTT	TCCCACGTTA	CGTAACTTCC	CATTTTAAGA	450
AAACTACAAT	TCCCAACACA	TACAAGTTAC	TCCGCCCTAA	AACCTACGTC	500
ACCCGCCCCG	TCCCCACGCC	CCGCGCCACG	TCACAACTC	CACCCCCTCA	550
TTATCATATT	GGCTTCAATC	CAAAATAAGG	TATATTATTG	ATGATGCTAG	600
CATCATCAAT	AATATACCTT	ATTTTGGATT	GAAGCCAATA	TGATAATGAG	650
GGGGTGGAGT	TTGTGACGTG	GCGCGGGGCG	TGGGAACGGG	GCGGGTGACG	700
TAGTAGTGTG	GCGGAAGTGT	GATGTTGCAA	GTGTGGCGGA	ACACATGTAA	750
GCGACGGATG	TGGCAAAGT	GACGTTTTTG	GTGTGCGCCG	GTGTACACAG	800
GAAGTGACAA	TTTTCGCGCG	GTTTTAGGCG	GATGTTGTAG	TAAATTTGGG	850
CGTAACCGAG	TAAGATTTGG	CCATTTTCGC	GGGAAACTG	AATAAGAGGA	900
AGTGAAATCT	GAATAATTTT	GTGTTACTCA	TAGCGCGTAA	TATTTGTCTA	950
GGGAGATCAG	CCTGCAGGTC	GTTACATAAC	TTACGGTAAA	TGGCCCGCCT	1000
GGCTGACCGC	CCAACGACCC	CCGCCCATTG	ACGTCAATAA	TGACGTATGT	1050
TCCCATAGTA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	TGGGTGGAGT	1100
ATTTACGGTA	AACTGCCCCAC	TTGGCAGTAC	ATCAAGTGTA	TCATATGCCA	1150
AGTACGCCCC	CTATTGACGT	CAATGACGGT	AAATGGCCCG	CCTGGCATTG	1200
TGCCCAGTAC	ATGACCTTAT	GGGACTTTCC	TACTTGGCAG	TACATCTACG	1250
TATTAGTCAT	CGCTATTACC	ATGGTGATGC	GGTTTTGGCA	GTACATCAAT	1300

CHIRITITI/TE CUEET /DIII E 261

11/45

FIGURE 5B

GGGCGTGGAT	AGCGGTTTGA	CTCACGGGGA	TTTCCAAGTC	TCCACCCCAT	1350
TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	GACTTTCCAA	1400
AATGTCGTAA	CAACTCCGCC	CCATTGACGC	AAATGGGCGG	TAGGCGTGTA	1450
CGGTGGGAGG	TCTATATAAG	CAGAGCTCGT	TTAGTGAACC	GTCAGATCGC	1500
CTGGAGACGC	CATCCACGCT	GTTTTGACCT	CCATAGAAGA	CACCGGGACC	1550
GATCCAGCCT	CCGGA CTCTA	GAGGATCCGG	TACTCGAGGA	ACTGAAAAAC	1600
CAGAAAGTTA	ACTGGTAAGT	TTAGTCTTTT	TGTCTTTTAT	TTCAGGTCCC	1650
GGATCCGGTG	GTGGTGCAA	TCAAAGA ACT	GCTCCTCAGT	GGATGTTGCC	1700
TTTACTTCTA	GGCCTGTACG	GAAGTGTTAC	TTCTGCTCTA	AAAGCTGCGG	1750
AATGTGATCC	GCGGCCGCAA	TTCCCGGGGA	TCGAAAGAGC	CTGCTAAAGC	1800
AAAAAAGAAG	TCACCATGTC	GTTTACTTTG	ACCAACAAGA	ACGTGATTTT	1850
CGTTGCCGGT	CTGGGAGGCA	TTGGTCTGGA	CACCAGCAAG	GAGCTGCTCA	1900
AGCGCGATCC	CGTCGTTTTA	CAACGTCGTG	ACTGGGAAAA	CCCTGGCGTT	1950
ACCCA ACTTA	ATCGCCTTGC	AGCACATCCC	CCTTTCGCCA	GCTGGCGTAA	2000
TAGCGAAGAG	GCCCCACCG	ATCGCCCTTC	CCAACAGTTG	CGCAGCCTGA	2050
ATGGCGAATG	GCGCTTTGCC	TGGTTTCCGG	CACCAGAAGC	GGTGCCGGAA	2100
AGCTGGCTGG	AGTGCGATCT	TCCTGAGGCC	GATACTGTCT	TCGTCCCCCTC	2150
AAACTGGCAG	ATGCACGGTT	ACGATGCGCC	CATCTACACC	AACGTAACCT	2200
ATCCCATTAC	GGTCAATCCG	CCGTTTGTTT	CCACGGAGAA	TCCGACGGGT	2250
TGTTACTCGC	TCACATTTAA	TGTTGATGAA	AGCTGGCTAC	AGGAAGGCCA	2300
GACGCGAATT	ATTTTGTGAT	GCGTTAACTC	GGCGTTTCAT	CTCTGGTGCA	2350
ACGGGCGCTG	GGTCGGTTAC	GGCCAGGACA	GTCGTTTGCC	GTCTGAATTT	2400
GACCTGAGCG	CATTTTACG	CGCCGGAGAA	AACCGCCTCG	CGGTGATGGT	2450
GCTGCGTTGG	AGTGACGGCA	GTTATCTGGA	AGATCAGGAT	ATGTGGCGGA	2500
TGAGCGGCAT	TTTCCGTGAC	GTCTCGTTGC	TGCATAAACC	GACTACACAA	2550
ATCAGCGATT	TCCATGTTGC	CACTCGCTTT	AATGATGATT	TCAGCCGCGC	2600

12/45

FIGURE 5C

TGTACTGGAG	GCTGAAGTTC	AGATGTGCGG	CGAGTTGCGT	GA CTACCTAC	2650
GGGTAACAGT	TTCTTTATGG	CAGGGTGAAA	CGCAGGTCGC	CAGCGGCACC	2700
GCGCCTTTCG	GCGGTGAAAT	TATCGATGAG	CGTGGTGGTT	ATGCCGATCG	2750
CGTCACACTA	CGTCTGAACG	TCGAAAACCC	GAAACTGTGG	AGCGCCGAAA	2800
TCCCCAATCT	CTATCGTGCG	GTGGTTGAAC	TGCACACCGC	CGACGGCACG	2850
CTGATTGAAG	CAGAAGCCTG	CGATGTGCGT	TTCCGCGAGG	TGCGGATTGA	2900
AAATGGTCTG	CTGCTGCTGA	ACGGCAAGCC	GTTGCTGATT	CGAGGCGTTA	2950
ACCGTCACGA	GCATCATCCT	CTGCATGGTC	AGGTCATGGA	TGAGCAGACC	3000
ATGGTG CAGG	ATATCCTGCT	GATGAAGCAG	AACAACTTTA	ACGCCGTGCG	3050
CTGTT CGCAT	TATCCGAACC	ATCCGCTGTG	GTACACGCTG	TGCGACCGCT	3100
ACGGCCTGTA	TGTGGTGGAT	GAAGCCAATA	TTGAAACCCA	CGGCATGGTG	3150
CCAATGAATC	GTCTGACCGA	TGATCCGCGC	TGGCTACCGG	CGATGAGCGA	3200
ACGCGTAACG	CGAATGGTGC	AGCGCGATCG	TAATCACCCG	AGTGTGATCA	3250
TCTGCTCGCT	GGGGAATGAA	TCAGGCCACG	GCGCTAATCA	CGACGCGCTG	3300
TATCGCTGGA	TCAAATCTGT	CGATCCTTCC	CGCCCGGTGC	AGTATGAAGG	3350
CGGCGGAGCC	GACACCACGG	CCACCGATAT	TATTTGCCCG	ATGTACGCGC	3400
GCGTGGATGA	AGACCAGCCC	TTCCCGGCTG	TGCCGAAATG	GTCCATCAAA	3450
AAATGGCTTT	CGCTACCTGG	AGAGACGCGC	CCGCTGATCC	TTTGCGAATA	3500
CGCCACGCG	ATGGGTAACA	GTCTTGGCGG	TTTCGCTAAA	TACTGGCAGG	3550
CGTTTCGTCA	GTATCCCCGT	TTACAGGGCG	GCTTCGTCTG	GGA CTGGGTG	3600
GATCAGTCGC	TGATTAAATA	TGATGAAAAC	GGCAACCCGT	GGTCGGCTTA	3650
CGGCGGTGAT	TTTGGCGATA	CGCCGAACGA	TCGCCAGTTC	TGTATGAACG	3700
GTCTGGTCTT	TGCCGACCGC	ACGCCGCATC	CAGCGCTGAC	GGAAGCAAAA	3750
CACCAGCAGC	AGTTTTTCCA	GTTCCGTTTA	TCCGGGCAAA	CCATCGAAGT	3800
GACCAGCGAA	TACCTGTTCC	GTCATAGCGA	TAACGAGCTC	CTGCACTGGA	3850
TGGTGGCGCT	GGATGGTAAG	CCGCTGGCAA	GCGGTGAAGT	GCCTCTGGAT	3900

SEQUENCE SHEET / PAGE 281

13/45

FIGURE 5D

GTCGCTCCAC AAGGTAAACA GTTGATTGAA CTGCCTGAAC TACCGCAGCC	3950
GGAGAGCGCC GGGCAACTCT GGCTCACAGT ACGCGTAGTG CAACCGAACG	4000
CGACCGCATG GTCAGAAGCC GGGCACATCA GCGCCTGGCA GCAGTGGCGT	4050
CTGGCGGAAA ACCTCAGTGT GACGCTCCCC GCGCGTCCC ACGCCATCCC	4100
GCATCTGACC ACCAGCGAAA TGGATTTTTG CATCGAGCTG GGTAATAAGC	4150
GTGGCAATT TAACCGCCAG TCAGGCTTTC TTTCACAGAT GTGGATTGGC	4200
GATAAAAAAC AACTGCTGAC GCCGCTGCGC GATCAGTTCA CCCGTGCACC	4250
GCTGGATAAC GACATTGGCG TAAGTGAAGC GACCCGATT GACCCTAACG	4300
CCTGGGTCGA ACGCTGGAAG GCGGCGGGCC ATTACCAGGC CGAAGCAGCG	4350
TTGTTGCAGT GCACGGCAGA TACACTTGCT GATGCGGTGC TGATTACGAC	4400
CGCTCACGCG TGGCAGCATC AGGGGAAAAC CTTATTTATC AGCCGGAAAA	4450
CCTACCGGAT TGATGGTAGT GGTCAAATGG CGATTACCGT TGATGTTGAA	4500
TGCGCGAGCG ATACACCGCA TCCGGCGCGG ATTGGCCTGA ACTGCCAGCT	4550
GGCGCAGGTA GCAGAGCGGG TAAACTGGCT CGGATTAGGG CCGCAAGAAA	4600
ACTATCCCGA CCGCCTTACT GCCGCCTGTT TTGACCGCTG GGATCTGCCA	4650
TTGTCAGACA TGTATACCCC GTACGTCTTC CCGAGCGAAA ACGGTCTGCG	4700
CTGCGGGACG CGCGAATTGA ATTATGGCCC ACACCAGTGG CGCGGCGACT	4750
TCCAGTTCOA CATCAGCCGC TACAGTCAAC AGCAACTGAT GGAAACCAGC	4800
CATCGCCATC TGCTGCACGC GGAAGAAGGC ACATGGCTGA ATATCGACGG	4850
TTTCCATATG GGGATTGGTG GCGACGACTC CTGGAGCCCG TCAGTATCGG	4900
CGGAATTACA GCTGAGCGCC GGTGCTACC ATTACCAGTT GGTCTGGTGT	4950
CAAAAATAAT AATAACCGGG CAGGCCATGT CTGCCCGTAT TTCGCGTAAG	5000
GAAATCCATT ATGTACTATT TAAAAAACAC AAACCTTTGG ATGTTCGGTT	5050
TATTCTTTTT CTTTTACTTT TTTATCATGG GAGCCTACTT CCCGTTTTTC	5100
CCGATTTGGC TACATGACAT CAACCATATC AGCAAAAGTG ATACGGGTAT	5150
TATTTTTGCC GCTATTTCTC TGTTCTCGCT ATTATTCCAA CCGCTGTTTG	5200
GTCTGCTTTC TGACAACTC GGCCTCGACT CTAGGCGGCC GCGGGGATCC	5250

14/45

FIGURE 5E

AGACATGATA	AGATACATTG	ATGAGTTTGG	ACAAACCACA	ACTAGAATGC	5300
AGTGAAAAAA	ATGCTTTATT	TGTGAAATTT	GTGATGCTAT	TGCTTTATTT	5350
GTAACCATTA	TAAGCTGCAA	TAAACAAGTT	AACAACAACA	ATTGCATTCA	5400
TTTTATGTTT	CAGGTTCAAG	GGGAGGTGTG	GGAGGTTTTT	TCGGATCCTC	5450
TAGAGTCGAC	GACGCGAGGC	TGGATGGCCT	TCCCCATTAT	GATTCTTCTC	5500
GCTTCCGGCG	GCATCGGGAT	GCCCGCGTTG	CAGGCCATGC	TGTCCAGGCA	5550
GGTAGATGAC	GACCATCAGG	GACAGCTTCA	AGGATCGCTC	GCGGCTCTTA	5600
CCAGCCTAAC	TTCGATCACT	GGACCGCTGA	TCGTACGGC	GATTTATGCC	5650
GCCTCGGCGA	GCACATGGAA	CGGGTTGGCA	TGGATTGTAG	GCGCCGCCCT	5700
ATACCTTGTC	TGCCTCCCCG	CGTTGCGTCG	CGGTGCATGG	AGCCGGGCCA	5750
CCTCGACCTG	AATGGAAGCC	GGCGGCACCT	CGCTAACGGA	TTCACTACTC	5800
CAAGAATTGG	AGCCAATCAA	TTCTTGCGGA	GAACTGTGAA	TGCGCAAACC	5850
AACCCTTGGC	AGAACATATC	CATCGCGTCC	GCCATCTCCA	GCAGCCGCAC	5900
GCGGCGCATC	TCGGGCAGCG	TTGGGTCCTG	GCCACGGGTG	CGCATGATCG	5950
TGCTCCTGTC	GTTGAGGACC	CGGCTAGGCT	GGCGGGGTTG	CCTTACTGGT	6000
TAGCAGAATG	AATCACCGAT	ACGCGAGCGA	ACGTGAAGCG	ACTGCTGCTG	6050
CAAAACGTCT	GCGACCTGAG	CAACAACATG	AATGGTCTTC	GGTTTCCGTG	6100
TTTCGTAAAG	TCTGGAAACG	CGGAAGTCAG	CGCCCTGCAC	CATTATGTTT	6150
CGGATCTGCA	TCGCAGGATG	CTGCTGGCTA	CCCTGTGGAA	CACCTACATC	6200
TGTATTAACG	AAGCCTTTCT	CAATGCTCAC	GCTGTAGGTA	TCTCAGTTTC	6250
GTGTAGGTCG	TTCGCTCCAA	GCTGGGCTGT	GTGCACGAAC	CCCCCGTTCA	6300
GCCCGACCGC	TGCGCCTTAT	CCGGTAACTA	TCGTCTTGAG	TCCAACCCGG	6350
TAAGACACGA	CTTATCGCCA	CTGGCAGCAG	CCACTGGTAA	CAGGATTAGC	6400
AGAGCGAGGT	ATGTAGGCGG	TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	6450
CTACGGCTAC	ACTAGAAGGA	CAGTATTTGG	TATCTGCGCT	CTGCTGAAGC	6500
CAGTTACCTT	CGGAAAAGA	GTTGGTAGCT	CTTGATCCGG	CAAACAAACC	6550

SEQUENCE LISTING

15/45

FIGURE 5F

ACCGCTGGTA	GCGGTGGTTT	TTTTGTTTGC	AAGCAGCAGA	TTACGCGCAG	6600
AAAAAAGGA	TCTCAAGAAG	ATCCTTTGAT	CTTTTCTACG	GGGTCTGACG	6650
CTCAGTGGAA	CGAAACTCA	CGTTAAGGGA	TTTTGGTCAT	GAGATTATCA	6700
AAAAGGATCT	TCACCTAGAT	CCTTTTAAAT	TA AAAATGAA	GTTTTAAATC	6750
AATCTAAAAGT	ATATATGAGT	AAACTTGGTC	TGACAGTTAC	CAATGCTTAA	6800
TCAGTGAGGC	ACCTATCTCA	GCGATCTGTC	TATTTCTGTC	ATCCATAGTT	6850
GCCTGACTCC	CCGTCGTGTA	GATAACTACG	ATACGGGAGG	GCTTACCATC	6900
TGGCCCCAGT	GCTGCAATGA	TACCGCGAGA	CCCACGCTCA	CCGGCTCCAG	6950
ATTTATCAGC	AATAAACCCAG	CCAGCCGGAA	GGGCCGAGCG	CAGAAGTGGT	7000
CCTGCAACTT	TATCCGCCTC	CATCCAGTCT	ATTAATTGTT	GCCGGGAAGC	7050
TAGAGTAAGT	AGTTCGCCAG	TTAATAGTTT	GCGCAACGTT	GTTGCCATTG	7100
CTGCAGGCAT	CGTGGTGTC	CGCTCGTCGT	TTGGTATGGC	TTCATTACAGC	7150
TCCGGTTCCC	AACGATCAAG	GCGAGTTACA	TCATCCCCCA	TGTTGTGCAA	7200
AAAAGCGGTT	AGCTCCTTCG	GTCCTCCGAT	CGTTGTCAGA	AGTAAGTTGG	7250
CCGCAGTGTT	ATCACTCATG	GTTATGCCAG	CACTGCATAA	TTCTCTTACT	7300
GTCATGCCAT	CCGTAAGATG	CTTTTCTGTG	ACTGGTGAGT	ACTCAACCAA	7350
GTCATTCTGA	GAATAGTGTA	TGCGGCGACC	GAGTTGCTCT	TGCCCCGGCGT	7400
CAACACGGGA	TAATACCGCG	CCACATAGCA	CAACTTTAAA	AGTGCTCATC	7450
ATTGGAAAAC	GTTCTTCGGG	GCGAAAACTC	TCAAGGATCT	TACCGCTGTT	7500
GAGATCCAGT	TCGATGTAA	CCACTCGTGC	ACCCAACTGA	TCTTCAGCAT	7550
CTTTTACTTT	CACCAGCGTT	TCTGGGTGAG	CAAAAACAGG	AAGGCAAAAT	7600
GCCGCAAAAA	AGGGAATAAG	GGCGACACGG	AAATGTTGAA	TACTCATACT	7650
CTTCCTTTTT	CAATATTATT	GAAGCATTTA	TCAGGGTTAT	TGTCTCATGA	7700
GCGGATACAT	ATTGAATGT	ATTAGAAAA	ATAAACAAAT	AGGGGTTCGG	7750
CGCACATTTT	CCCGAAAAGT	GCCACCTGAC	GTCTAAGAAA	CCATTATTAT	7800
CATGACATTA	ACCTATAAAA	ATAGGCGTAT	CACGAGGCCC	TTTCGTCCTC	7850
AA					7852

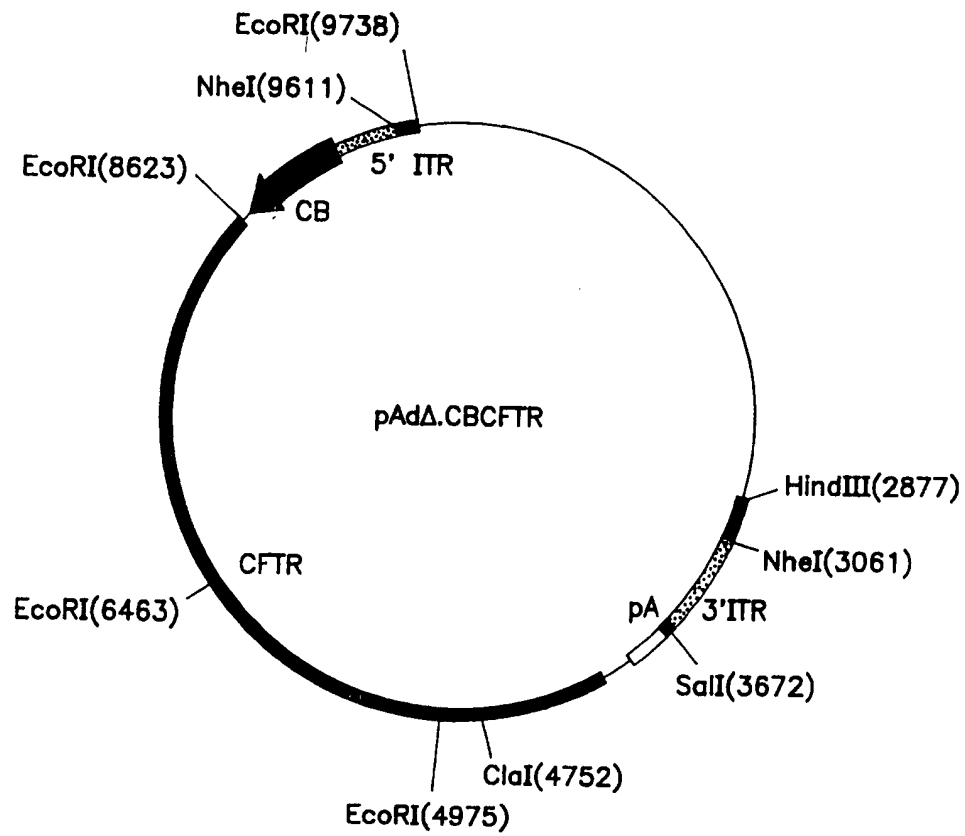


FIG. 6

SUBSTITUTE SHEET (RULE 26)

17/45

FIGURE 7A

TCTTCCGCTT CCTCGCTCAC TGA	CTCGCTG CGCTCGGTCG TTCGGCTGCG	50
GCGAGCGGTA TCAGCTCACT CAAAGGCGGT	AATACGGTTA TCCACAGAAT	100
CAGGGGATAA CGCAGGAAAG AACATGTGAG	CAAAAGGCCA GCAAAAGGCC	150
AGGAACCGTA AAAAGGCCGC GTTGCTGGCG	TTTTTCCATA GGCTCCGCCC	200
CCCTGACGAG CATCACAAAA ATCGACGCTC	AAGTCAGAGG TGGCGAAACC	250
CGACAGGACT ATAAAGATAC CAGGCGTTTC	CCCCTGGAAG CTCCCTCGTG	300
CGCTCTCCTG TTCCGACCCT GCCGCTTACC	GGATACCTGT CCGCCTTTCT	350
CCCTTCGGGA AGCGTGGCGC TTTCTCATAG	CTCACGCTGT AGGTATCTCA	400
GTTCGGTGTA GGTCGTTCGC TCCAAGCTGG	GCTGTGTGCA CGAACCCCCC	450
GTTCAGCCCG ACCGCTGCGC CTTATCCGGT	AACTATCGTC TTGAGTCCAA	500
CCCGGTAAGA CACGACTTAT CGCCACTGGC	AGCAGCCACT GGTAACAGGA	550
TTAGCAGAGC GAGGTATGTA GGCGGTGCTA	CAGAGTTCTT GAAGTGGTGG	600
CCTAACTACG GCTACACTAG AAGAACAGTA	TTTGGTATCT GCGCTCTGCT	650
GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG	TAGCTCTTGA TCCGGCAAAC	700
AAACCACCGC TGGTAGCGGT GGTTTTTTTG	TTTGCAAGCA GCAGATTACG	750
CGCAGAAAAA AAGGATCTCA AGAAGATCCT	TTGATCTTTT CTACGGGGTC	800
TGACGCTCAG TGGAACGAAA ACTCACGTTA	AGGGATTTTG GTCATGAGAT	850
TATCAAAAAG GATCTTCACC TAGATCCTTT	TAAATTAAAA ATGAAGTTTT	900
AAATCAATCT AAAGTATATA TGAGTAACT	TGGTCTGACA GTTACCAATG	950
CTTAATCAGT GAGGCACCTA TCTCAGCGAT	CTGTCTATTT CGTTCATCCA	1000
TAGTTGCCTG ACTCCCCGTC GTGTAGATAA	CTACGATACG GGAGGGCTTA	1050
CCATCTGGCC CCAGTGCTGC AATGATACCG	CCAGACCCAC GCTCACCGGC	1100
TCCAGATTTA TCAGCAATAA ACCAGCCAGC	CGGAAGGGCC GAGCGCAGAA	1150
GTGGTCCTGC AACTTTATCC GCCTCCATCC	AGTCTATTAA TTGTTGCCGG	1200
GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT	AGTTTGCGCA ACGTTGTTGC	1250
CATTGCTACA GGCATCGTGG TGTCACGCTC	GTCGTTTGGT ATGGCTTCAT	1300

18/45

FIGURE 7B

TCAGCTCCGC	TTCCCAACGA	TCAAGGCGAG	TTACATGATC	CCCCATGTTG	1350
TGCAAAAAAG	CGGTTAGCTC	CTTCGGTCCT	CCGATCGTTG	TCAGAAGTAA	1400
GTTGGCCGCA	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC	1450
TTACTGTCAT	GCCATCCGTA	AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	1500
ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	CGACCGAGTT	GCTCTTGCCC	1550
GGCGTCAATA	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	TTAAAAGTGC	1600
TCATCATTGG	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	GATCTTACCG	1650
CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA	ACTGATCTTC	1700
AGCATCTTTT	ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	1750
AAAATGCCGC	AAAAAAGGGA	ATAAGGGCGA	CACGGAAATG	TTGAATACTC	1800
ATACTCTTCC	TTTTTCAATA	TTATTGAAGC	ATTTATCAGG	GTTATTGTCT	1850
CATGAGCGGA	TACATATTTG	AATGTATTTA	GAAAAATAAA	CAAATAGGGG	1900
TTCCGCGCAC	ATTTCCCCGA	AAAGTGCCAC	CTGACGTCTA	AGAAACCATT	1950
ATTATCATGA	CATTAACCTA	TAAAAATAGG	CGTATCACGA	GGCCCTTTTCG	2000
TCTCGCGCGT	TCGGGTGATG	ACGGTGAAAA	CCTCTGACAC	ATGCAGCTCC	2050
CGGAGACGGT	CACAGCTTGT	CTGTAAGCGG	ATGCCGGGAG	CAGACAAGCC	2100
CGTCAGGGCG	CGTCAGCGGG	TGTTGGCGGG	TGTCGGGGCT	GGCTTAACTA	2150
TGCGGCATCA	GAGCAGATTG	TACTGAGAGT	GCACCATAAA	ATTGTAAACG	2200
TTAATATTTT	GTAAAAATTC	GCGTTAAATT	TTTGTTAAAT	CAGCTCATTT	2250
TTTAACCAAT	AGGCCGAAAT	CGGCAAAATC	CCTTATAAAT	CAAAAGAATA	2300
GCCCGAGATA	GGGTTGAGTG	TTGTTCCAGT	TTGGAACAAG	AGTCCACTAT	2350
TAAAGAACGT	GGACTCCAAC	GTCAAAGGGC	GAAAAACCGT	CTATCAGGGC	2400
GATGGCCAC	TACGTGAACC	ATCACCCTAA	TCAAGTTTTC	TGGGGTCGAG	2450
GTGCCGTAAA	GCACTAAATC	GGAACCCTAA	AGGGAGCCCC	CGATTTAGAG	2500
CTTGACGGGG	AAAGCCGGCG	AACGTGGCGA	GAAAGGAAGG	GAAGAAAGCG	2550
AAAGGAGCGG	GCGCTAGGGC	GCTGGCAAGT	GTAGCGGTCA	CGCTGCGCGT	2600

SUBSTITUTE SHEET (RULE 5.2)

FIGURE 7C

AACCACCACA	CCCGCCGCGC	TTAATGCGCC	GCTACAGGGC	GCGTACTATG	2650
GTTGCTTTGA	CGTATGCGGT	GTGAAATACC	GCACAGATGC	GTAAGGAGAA	2700
AATACCGCAT	CAGGCGCCAT	TCGCCATTCA	GGCTGCGCAA	CTGTTGGGAA	2750
GGGCGATCGG	TGCGGGCCTC	TTCGCTATTA	CGCCAGCTGG	CGAAAGGGGG	2800
ATGTGCTGCA	AGGCGATTAA	GTTGGGTAAC	GCCAGGGTTT	TCCAGTCAC	2850
GACGTTGTAA	AACGACGGCC	AGTGCCAAGC	TTAAGGTGCA	CGGCCCACGT	2900
GGCCACTAGT	ACTTCTCGAG	CTCTGTACAT	GTCCGCGGTC	GCGACGTACG	2950
CGTATCGATG	GCGCCAGCTG	CAGGCGGCCG	CCATATGCAT	CCTAGGCCTA	3000
TTAATATTCC	GGAGTATACG	TAGCCGGCTA	ACGTTAACAA	CCGGTACCTC	3050
TAGAACTATA	GCTAGCCAAT	TCCATCATCA	ATAATATACC	TTATTTTGGA	3100
TTGAAGCCAA	TATGATAATG	AGGGGGTGGA	GTTTGTGACG	TGGCGCGGGG	3150
CGTGGAACG	GGGCGGGTGA	CGTAGGTTTT	AGGGCGGAGT	AACTTGTATG	3200
TGTTGGGAAT	TGTAGTTTTC	TTAAAATGGG	AAGTTACGTA	ACGTGGGAAA	3250
ACGGAAGTGA	CGATTTGAGG	AAGTTGTGGG	TTTTTTGGCT	TCGTTTCTC	3300
GGCGTAGGTT	CGCGTGCGGT	TTCTGGGTG	TTTTTTGTGG	ACTTTAACCG	3350
TTACGTCATT	TTTTAGTCCT	ATATATACTC	GCTCTGCACT	TGGCCCTTTT	3400
TTACACTGTG	ACTGATTGAG	CTGCTGCCGT	GTCGACTGGT	GTTTTTTTAA	3450
TAGGTTTTCT	TTTTTACTGG	TAAGGCTGAC	TGTTAGGCTG	CCGCTGTGAA	3500
GCGCTGTATG	TTGTTCTGGA	GCGGGAGGGT	GCTATTTTGC	CTAGGCAGGA	3550
GGGTTTTTCA	GGTGTTTATG	TGTTTTTCTC	TCCTATTAAT	TTTGTTATAC	3600
CTCCTATGGG	GGCTGTAATG	TTGTCTCTAC	GCCTGCGGGT	ATGTATTCCC	3650
CCCAAGCTTG	CATGCCTGCA	GGTCGACTCT	AGAGGATCCG	AAAAAACCTC	3700
CCACACCTCC	CCCTGAACCT	GAAACATAAA	ATGAATGCAA	TTGTTGTTGT	3750
TAACTTGTTT	ATTGCAGCTT	ATAATGGTTA	CAAATAAAGC	AATAGCATCA	3800
CAAATTTTCA	AAATAAAGCA	TTTTTTTTCAC	TGCATTCTAG	TTGTGGTTTG	3850
TCCAAACTCA	TCAATGTATC	TTATCATGTC	TGGATCCCCC	TAGCTTGCCA	3900

20/45

FIGURE 7D

AACCTACAGG	TGGGGTCTTT	CATCCCCC	TTTTTCTGGA	GACTAAATAA	3950
AATCTTTTAT	TTTATCTATG	GCTCGTACTC	TATAGGCTTC	AGCTGGTGAT	4000
ATTGTTGAGT	CAAACTAGA	GCCTGGACCA	CTGATATCCT	GTCTTTAACA	4050
AATTGGACTA	ATCGCGGGAT	CAGCCAATTC	CATGAGCAAA	TGTCCCATGT	4100
CAACATTTAT	GCTGCTCTCT	AAAGCCTTGT	ATCTTGCATC	TCTTCTTCTG	4150
TCTCCTCTTT	CAGAGCAGCA	ATCTGGGGCT	TAGACTTGCA	CTTGCTTGAG	4200
TTCCGGTGGG	GAAAGAGCTT	CACCCTGTCT	GAGGGGCTGA	TGGCTTGCCG	4250
GAAGAGGCTC	CTCTCGTTCA	GCAGTTTCTG	GATGGAATCG	TACTGCCGCA	4300
CTTTGTTCTC	TTCTATGACC	AAAAATTGTT	GGCATTCCAG	CATTGCTTCT	4350
ATCCTGTGTT	CACAGAGAAT	TACTGTGCAA	TCAGCAAATG	CTTGTTTTAG	4400
AGTTCTTCTA	ATTATTTGGT	ATGTTACTGG	ATCCAAATGA	GCACTGGGTT	4450
CATCAAGCAG	CAAGATCTTC	GCCTTACTGA	GAACAGATCT	AGCCAAGCAC	4500
ATCAACTGCT	TGTGGCCATG	GCCTTAGGACA	CAGCCCCCAT	CCACAAGGAC	4550
AAAGTCAAGC	TTCCAGGAA	ACTGTTCTAT	CACAGATCTG	AGCCCAACCT	4600
CATCTGCAAC	TTTCCATATT	TCTTGATCAC	TCCACTGTTC	ATAGGGATCC	4650
AAGTTTTTTC	TAAATGTTCC	AGAAAAATA	AATACTTTCT	GTGGTATCAC	4700
TCCAAAGGCT	TTCTCCACT	GTTGCAAAGT	TATTGAATCC	CAAGACACAC	4750
CATCGATCTG	GATTTCTCCT	TCAGTGTTC	GTAAGTCTCA	AAAAGCTGAT	4800
AACAAAGTAC	TCTTCCCTGA	TCCAGTTCTT	CCCAAGAGGC	CCACCCTCTG	4850
GCCAGGACTT	ATTGAGAAGG	AAATGTTCTC	TAATATGGCA	TTTCCACCTT	4900
CTGTGTATTT	TGCTGTGAGA	TCTTTGACAG	TCATTTGGCC	CCCTGAGGGC	4950
CAGATGTCAT	CTTCTTTCAC	GTGTGAATTC	TCAATAATCA	TAACTTTCTG	5000
GAGTTGGCCA	TTCTTGATG	GTTTGGTTGA	CTTGGTAGGT	TTACCTTCTG	5050
TTGGCATGTC	AATGAACTTA	AAGACTCGGC	TCACAGATCG	CATCAAGCTA	5100
TCCACATCTA	TGCTGGAGTT	TACAGCCAC	TGCAATGTAC	TCATGATATT	5150
CATGGCTAAA	GTCAGGATAA	TACCAACTCT	TCCTTCTCCT	TCTCCTGTTG	5200

SEQUENCE SHEET / PAGE 92\

21/45

FIGURE 7E

TTAAATGGA	AATGAAGGTA	ACAGCAATGA	AGAAGATGAC	AAAAATCATT	5250
TCTATTCTCA	TTTGAACCA	GCGCAGTGTT	GACAGGTACA	AGAACCAGTT	5300
GGCAGTATGT	AAATTCAGAG	CTTTGTGGAA	CAGAGTTTCA	AAGTAAGGCT	5350
GCCGTCCGAA	GGCACGAAGT	GTCCATAGTC	CTTTTAAGCT	TGTAACAAGA	5400
TGAGTGAAAA	TTGGACTCCT	GCCTTCAGAT	TCCAGTTGTT	TGAGTTGCTG	5450
TGAGGTTTGG	AGGAAATATG	CTCTCAACAT	AATAAAAGCC	ACTATCACTG	5500
GCACTGTTGC	AACAAAGATG	TAGGGTTGTA	AACTGCGAC	AACTGCTATA	5550
GCTCCAATCA	CAATTAATAA	CAACTGGATG	AAGTCAAATA	TGGTAAGAGG	5600
CAGAAGGTCA	TCCAAAATTG	CTATATCTTT	GGAGAATCTA	TTAAGAATCC	5650
CACCTGCTTT	CAACGTGTTG	AGGGTTGACA	TAGGTGCTTG	AAGAACAGAA	5700
TGTAACATTT	TGTGGTGTA	AATTTTCGAC	ACTGTGATTA	GAGTATGCAC	5750
CAGTGGTAGA	CCTCTGAAGA	ATCCCATAGC	AAGCAAAGTG	TCGGCTACTC	5800
CCACGTAAAT	GTAAACACA	TAATACGAAC	TGGTGCTGGT	GATAATCACT	5850
GCATAGCTGT	TATTTCTACT	ATGAGTACTA	TTCCCTTTGT	CTTGAAGAGG	5900
AGTGTTCCTCA	AGGAGCCACA	GCACAACCAA	AGAAGCAGCC	ACCTCTGCCA	5950
GAAAAATTAC	TAAGCACCAA	ATTAGCACAA	AAATTAAGCT	CTTGTGGACA	6000
GTAATATATC	GAAGGTATGT	GTTCCATGTA	GTCAGTCTG	GTATGCTCTC	6050
CATATCATCA	AAAAAGCACT	CCTTTAAGTC	TTCTTCGTTA	ATTTCTTCAC	6100
TTATTTCCAA	GCCAGTTTCT	TGAGATAACC	TTCTTGAATA	TATATCCAGT	6150
TCAGTCAAGT	TTGCCTGAGG	GGCCAGTGAC	ACTTTTCGTG	TGGATGCTGT	6200
TGTCTTTCGG	TGAATGTTCT	GACCTTGGTT	AACTGAGTGT	GTCATCAGGT	6250
TCAGGACAGA	CTGCCTCCTT	CGTGCCTGAA	GCGTGGGGCC	AGTGCTGATC	6300
ACGCTGATGC	GAGGCAGTAT	CGCCTCTCCC	TGCTCAGAAT	CTGGTACTAA	6350
GGACAGCCTT	CTCTCTAAAG	GCTCATCAGA	ATCCTCTTCG	ATGCCATTCA	6400
TTTGTAAGGG	AGTCTTTTGC	ACAATGGAAA	ATTTTCGTAT	AGAGTTGATT	6450
GGATTGAGAA	TAGAATTCTT	CCTTTTTTCC	CCAAACTCTC	CAGTCTGTTT	6500

22/45

FIGURE 7F

AAAAGATTGT	TTTTTTGTTT	CTGTCCAGGA	GACAGGAGCA	TCTCCTTCTA	6550
ATGAGAAACG	GTGTAAGGTC	TCAGTTAGGA	TTGAATTTCT	TCTTTCTGCA	6600
CTAAATTGGT	CGAAAGAATC	ACATCCCATG	AGTTTTGAGC	TAAAGTCTGG	6650
CTGTAGATTT	TGGAGTTCTG	AAAATGTCCC	ATAAAAATAG	CTGCTACCTT	6700
CATGCAAAAT	TAATATTTTG	TCAGCTTTCT	TTAAATGTTC	CATTTTAGAA	6750
GTGACCAAAA	TCCTAGTTTT	GTTAGCCATC	AGTTTACAGA	CACAGCTTTC	6800
AAATATTTCT	TTTTCTGTTA	AAACATCTAG	GTATCCAAAA	GGAGAGTCTA	6850
ATAAATACAA	ATCAGCATCT	TTGTATACTG	CTCTTGCTAA	AGAAATTCTT	6900
GCTCGTTGAC	CTCCACTCAG	TGTGATTCCA	CCTTCTCCAA	GAACATATTT	6950
GTCTTTCTCT	GCAAACTTGG	AGATGTCCTC	TTCTAGTTGG	CATGCTTTGA	7000
TGACGCTTCT	GTATCTATAT	TCATCATAGG	AAACACCAAA	GATGATATTT	7050
TCTTTAATGG	TGCCAGGCAT	AATCCAGGAA	AACTGAGAAC	AGAATGAAAT	7100
TCTTCCACTG	TGCTTAATTT	TACCCTCTGA	AGGCTCCAGT	TCTCCCATAA	7150
TCATCATTAG	AAGTGAAGTC	TTGCCTGCTC	CAGTGGATCC	AGCAACCGCC	7200
AACAACTGTC	CTCTTTCTAT	CTTGAAATTA	ATATCTTTCA	GGACAGGAGT	7250
ACCAAGAAGT	GAGAAATTAC	TGAAGAAGAG	GCTGTCATCA	CCATTAGAAG	7300
TTTTTCTATT	GTTATTGTTT	TGTTTTGCTT	TCTCAAATAA	TTCCCCAAAT	7350
CCCTCCTCCC	AGAAGGCTGT	TACATTCTCC	ATCACTACTT	CTGTAGTCGT	7400
TAAGTTATAT	TCCAATGTCT	TATATTCTTG	CTTTTGTAAG	AAATCCTGTA	7450
TTTTGTTTAT	TGCTCCAAGA	GAGTCATACC	ATGTTTGTAAC	AGCCCAGGGA	7500
AATTGCCGAG	TGACCGCCAT	GCGCAGAACA	ATGCAGAATG	AGATGGTGGT	7550
GAATATTTTC	CGGAGGATGA	TTCTTTTGAT	TAGTGCATAG	GGAAGCACAG	7600
ATAAAACAC	CACAAAGAAC	CCTGAGAAGA	AGAAGGCTGA	GCTATTGAAG	7650
TATCTCACAT	AGGCTGCCTT	CCGAGTCAGT	TTGAGTTCTG	TTTGTCTTAA	7700
GTTTTCAATC	ATTTTTTCCA	TTGCTTCTTC	CCAGCAGTAT	GCCTTAACAG	7750
ATTGGATGTT	CTCGATCATT	TCTGAGGTAA	TCACAAGTCT	TTCACTGATC	7800

SEQUENCE LISTING

23/45

FIGURE 7G

TTCCCAGCTC	TCTGATCTCT	GTACTTCATC	ATCATTCTCC	CTAGCCCAGC	7850
CTGAAAAAGG	GCAAGGACTA	TCAGGAAACC	AAGTCCACAG	AAGGCAGACG	7900
CCTGTAACAA	CTCCCAGATT	AGCCCCATGA	GGAGTGCCAC	TTGCAAAGGA	7950
GCGATCCACA	CGAAATGTGC	CAATGCAAGT	CCTTCATCAA	ATTTGTTTCAG	8000
GTGTTGGAA	AGGAGACTAA	CAAGTTGTCC	AATACTTATT	TTATCTAGAA	8050
CACGGCTTGA	CAGCTTTAAA	GTCTTCTTAT	AAATCAAAC	AAACATAGCT	8100
ATTCTCATCT	GCATTCCAAT	GTGATGAAGG	CCAAAAATGG	CTGGGTGTAG	8150
GAGCAGTGTC	CTCACAATAA	AGAGAAGGCA	TAAGCCTATG	CCTAGATAAA	8200
TCGCGATAGA	GCGTTCCTCC	TTGTTATCCG	GGTCATAGGA	AGCTATGATT	8250
CTTCCCAGTA	AGAGAGGCTG	TACTGCTTTG	GTGACTTCCC	CTAAATATAA	8300
AAAGATTCCA	TAGAACATAA	ATCTCCAGAA	AAAACATCGC	CGAAGGGCAT	8350
TAATGAGTTT	AGGATTTTTT	TTTGAAGCCA	GCTCTCTATC	CCATTCTCTT	8400
TCCAATTTTT	CAGATAGATT	GTGAGAGCAA	TCAACAGAAG	GGATTTGGTA	8450
TATGTCTGAC	AATTCCAGGC	GCTGTCTGTA	TCCTTTCCTC	AAAATTGGTC	8500
TGGTCCAGCT	GAAAAAAGT	TTGGAGACAA	CGCTGGCCTT	TTCCAGAGGC	8550
GACCTCTGCA	TGGTCTCTCG	GGCGCTGGGG	TCCCTGCTAG	GGCCGTCTGG	8600
GCTCAAGCTC	CTAATGCCAA	AGGAATTCCT	GCAGCCCGGG	GGATCCACTA	8650
GTTCTAGAGC	GGCCGCCACC	GCGGTGGCTG	ATCCCGCTCC	CGCCCGCCGC	8700
GCGCTTCGCT	TTTTATAGGG	CCGCCGCCGC	CGCCGCCTCG	CCATAAAAGG	8750
AAACTTTCGG	AGCGCGCCGC	TCTGATTGGC	TGCCGCCGCA	CCTCTCCGCC	8800
TCGCCCCGCC	CCGCCCTCG	CCCCGCCCG	CCCCGCCTGG	CGCGCGCCCC	8850
CCCCCCCCC	CCGCCCCAT	CGCTGCACAA	AATAATTAAA	AAATAAATAA	8900
ATACAAAATT	GGGGGTGGGG	AGGGGGGGGA	GATGGGGAGA	GTGAAGCAGA	8950
ACGTGGCCTC	GAGTAGATGT	ACTGCCAAGT	AGGAAAGTCC	CATAAGGTCA	9000
TGTACTGGGC	ATAATGCCAG	GCGGGCCATT	TACCGTCATT	GACGTCAATA	9050
GGGGGCGTAC	TTGGCATATG	ATACACTTGA	TGTACTGCCA	AGTGGGCAGT	9100

24/45

FIGURE 7H

TTACCGTAAA TACTCCACCC ATTGACGTCA ATGGAAAGTC CCTATTGGCG	9150
TTACTATGGG AACATACGTC ATTATTGACG TCAATGGGCG GGGGTCGTTG	9200
GGCGGTCAGC CAGGCGGGCC ATTTACCGTA AGTTATGTAA CGACCTGCAG	9250
GCTGATCTCC CTAGACAAAT ATTACGCGCT ATGAGTAACA CAAAATTATT	9300
CAGATTTTAC TTCCTCTTAT TCAGTTTTCC CGCGAAAATG GCCAAATCTT	9350
ACTCGGTTAC GCCCAAATTT ACTACAACAT CCGCCTAAAA CCGCGCGAAA	9400
ATTGTCACCTT CCTGTGTACA CCGGCGCACA CCAAAAACGT CACTTTTGCC	9450
ACATCCGTCG CTTACATGTG TTCCGCCACA CTTGCAACAT CACACTTCCG	9500
CCACACTACT ACGTCACCCG CCCCGTTCCC ACGCCCCGCG CCACGTCACA	9550
AACTCCACCC CCTCATTATC ATATTGGCTT CAATCCAAAA TAAGGTATAT	9600
TATTGATGAT GCTAGCATGC GCAAATTTAA AGCGCTGATA TCGATCGCGC	9650
GCAGATCTGT CATGATGATC ATTGCAATTG GATCCATATA TAGGGCCCGG	9700
GTTATAATTA CCTCAGGTCG ACGTCCCATG GCCATTGCGA TTCGTAATCA	9750
TGGTCATAGC TGTTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA	9800
CAACATACGA GCCGGAAGCA TAAAGTGTA AGCCTGGGGT GCCTAATGAG	9850
TGAGCTAACT CACATTAATT GCGTTGCGCT CACTGCCCCG TTTCCAGTCG	9900
GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG	9950
AGGCGGTTTG CGTATTGGGC GC	9972

SEQUENCE LISTING (CONTINUED)

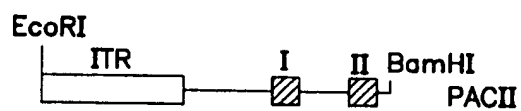


FIG. 8A

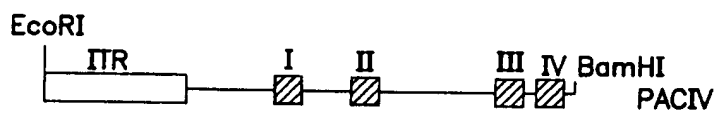


FIG. 8B

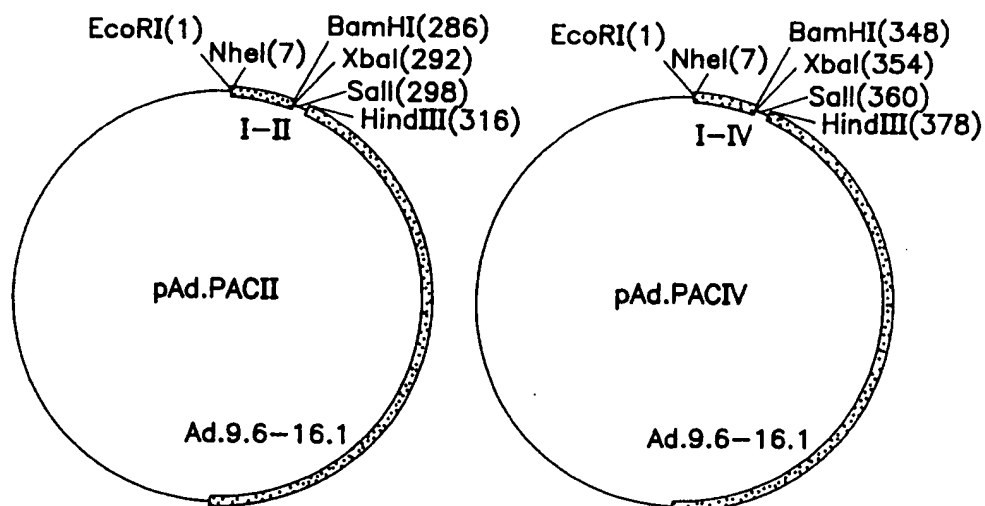
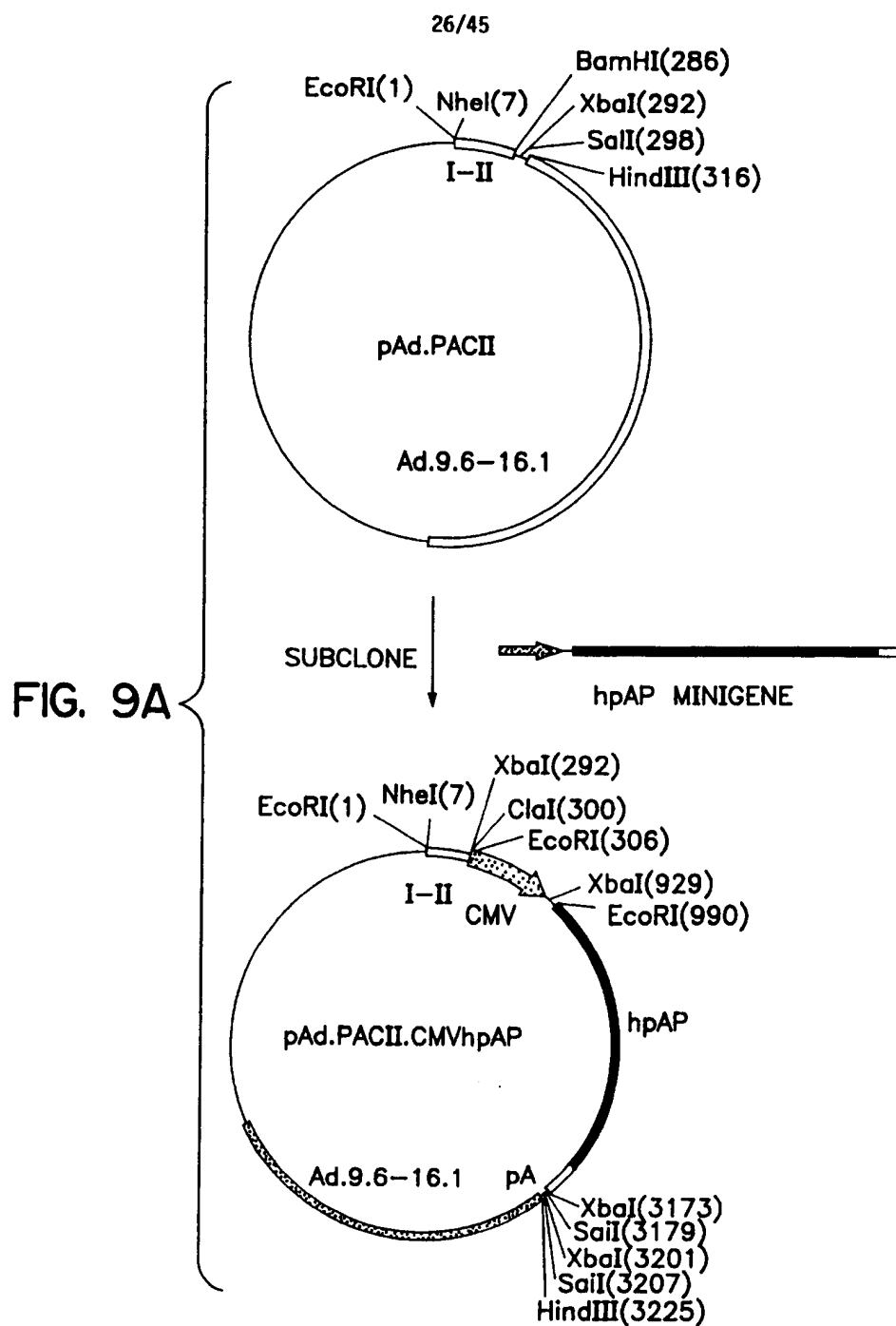


FIG. 8C



REPRODUCED FROM THE P. 221

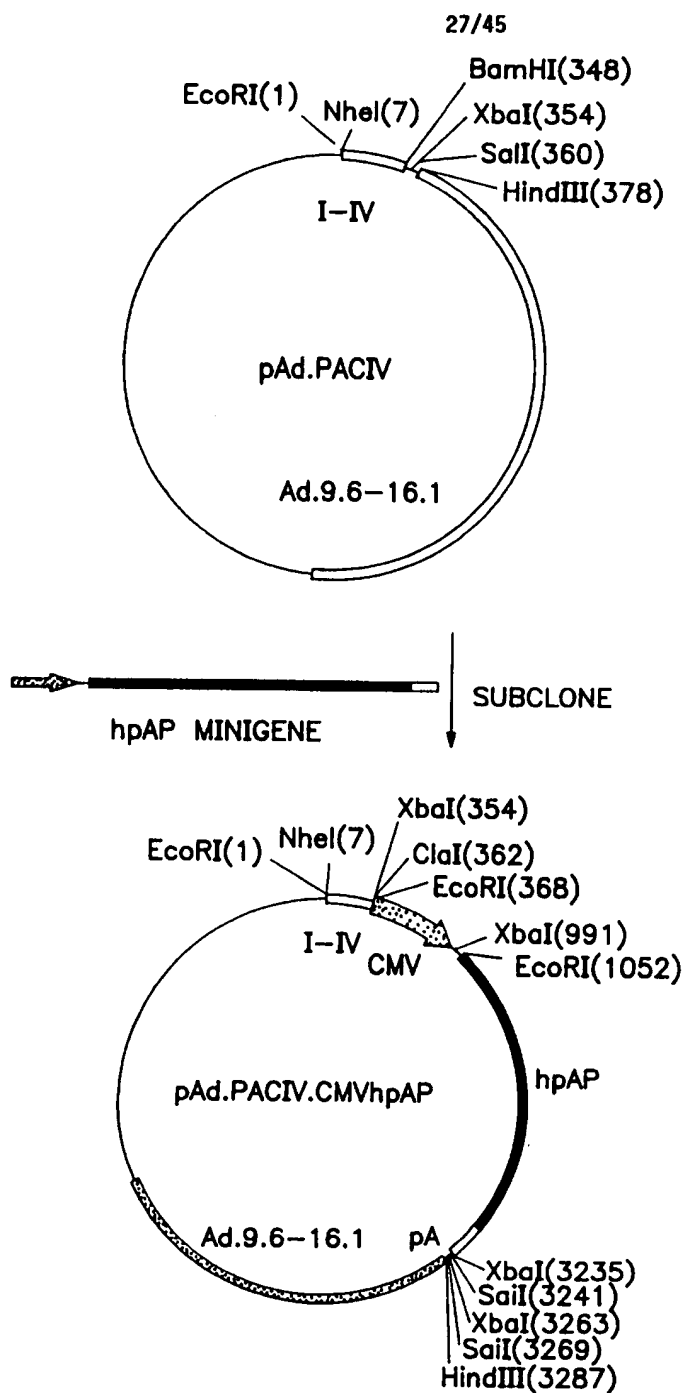
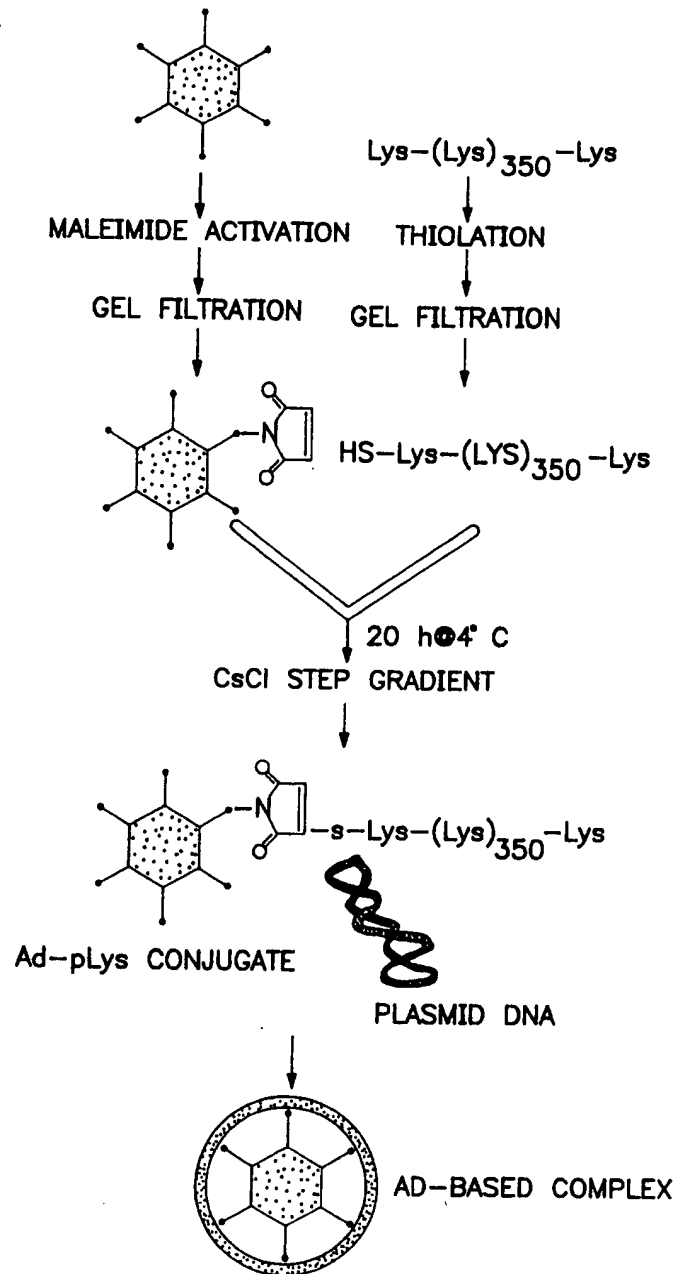


FIG. 9B

28/45

FIG. 10



PROTEIN EXPRESSION

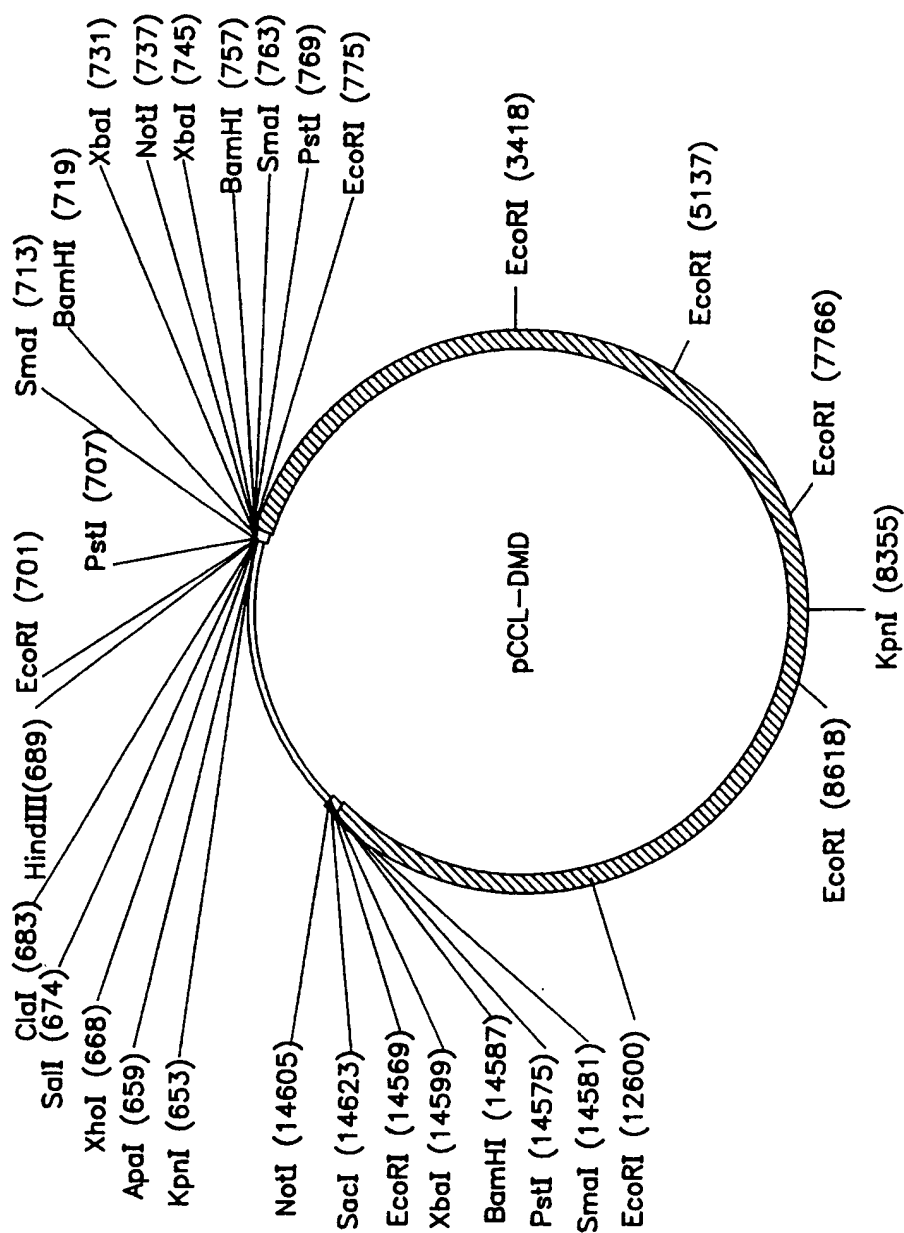


FIG. 11

30/45

FIGURE 12A

CCAATTCCAT	CATCAATAAT	ATACCTTATT	TTGGATTGAA	GCCAATATGA	50
TAATGAGGGG	GTGGAGTTTG	TGACGTGGCG	CGGGGCGTGG	GAACGGGGCG	100
GGTGACGTAG	GTTTtagggc	GGAGTAACTT	GTATGTGTTG	GGAATTGTAG	150
TTTTCTTAAA	ATGGGAAGTT	ACGTAACGTG	GGAAAACGGA	AGTGACGATT	200
TGAGGAAGTT	GTGGGTTTTT	TGGCTTTCGT	TTCTGGGCGT	AGGTTGCGGT	250
GCGGTTTTCT	GGGTGTTTTT	TGTGGACTTT	AACCGTTACG	TCATTTTTTA	300
GTCCTATATA	TACTCGCTCT	GCACTTGGCC	CTTTTTTACA	CTGTGACTGA	350
TTGAGCTGGT	GCCGTGTCGA	GTGGTGTTTT	TTTAATAGGT	TTTCTTTTTT	400
ACTGGTAAGG	CTGACTGTTA	GGCTGCCGCT	GTGAAGCGCT	GTATGTTGTT	450
CTGGAGCGGG	AGGGTGCTAT	TTTGCCTAGG	CAGGAGGGTT	TTTCAGGTGT	500
TTATGTGTTT	TTCTCTCCTA	TTAATTTTGT	TATACCTCCT	ATGGGGGCTG	550
TAATGTTGTC	TCTACGCCTG	CGGGTATGTA	TTCCCCCAA	GCTTGCATGC	600
CTGCAGGTCG	ACTCTAGAGG	ATCCGAAAAA	ACCTCCCACA	CCTCCCCCTG	650
AACCTGAAAC	ATAAAATGAA	TGCAATTGTT	GTTGTAACT	TGTTTATTGC	700
AGCTTATAAT	GGTTACAAAT	AAAGCAATAG	CATCACAAAT	TTCACAAATA	750
AAGCATTTTT	TTCACTGCAT	TCTAGTTGTG	GTTTGTCCAA	ACTCATCAAT	800
GTATCTTATC	ATGTCTGGAT	CCCCGCGGCC	GCTCTAGAAC	TAGTGGATCC	850
CCCCGGCTGC	AGGAATTCCG	TAACATAACT	GCGTGCTTTA	TTGAGATACA	900
CAGTAAAGCA	GTAATATAAT	ACAATAGTAA	GGCATATATT	TGGTGAAATC	950
TGATATGTTG	TGAAAATGCA	GTAAACTGA	AGTTTAAAAA	AATAATTAGT	1000
AAATGTTACA	GTGTTGGTGT	TAAAACACAA	TCTATTATGA	TACTCAAGTA	1050
AGAGTCCAGT	ACCTGGAGAC	AATGATGATA	CATGCCATGT	GATGATTATG	1100
CTTCAGTTAC	ACTGATTATG	ATTTACACTT	TAATACTTGA	TGGTTATAAA	1150
GAACATGAAA	TGATGTCCAA	ATTATGCTTA	AAATCAGCAA	TAAAGCTCTC	1200
AGTTTTTATT	CAAATATTTT	GATAGATTCA	CTCCAGAACT	AATATCTAAA	1250

ATTACTGTTTGT AGTCTTATGA TACTCAAGTA

FIGURE 12B

AGATAAAACG AAAAGATTAA AACAAAAC TA GCACTCTAT CTACCTTGGA	1300
TTT TAGAATG AAAC TTAAAA CTTCTTAGTA GGAAAGGAAC CCCTTGTTTT	1350
AAATCTTGGT GAAAACAAAT CCTTGGATAA AGAAAATGCC CAGTGCCACA	1400
TAAAGGAGAG AGAGAGAGAA AAGCAAGACC AGAACCAAAT TTCAATTTGT	1450
TATCTTAGAG CTTTGGGTTT TCTTTTGGA ATTATAAATG AAAAAAGGAA	1500
ACTGGTGTCC ACACAACAGA CAAGTGGTGA AGTTGTGAAA TTAGGTGTGC	1550
ACAATTACTA GAAACACCCC AAAACCAAAG TGAGGTAGAA ATAGCATGAG	1600
AAGCTGTGTT TGATGTTAAT TACAATTAAT AATGGACAAA ACCCACTCGC	1650
TAGAAGTTAA TTACACTTGA CGTTAGAGGT AACAGATTG CAAAATGATA	1700
GGACAGTGAT TTCTATTGAG AGAATGCTCT TTAAATGCTA AGAAGAAGAA	1750
ACTGGCATGA GAGGAGTAA GCTCTTCCTA GCAGTCCTTA GCTTTCTGTT	1800
GCAC TTTTTC TCCTGGTTCA ATGACTTGCA TTTGTTTAGA CATTTCAGCC	1850
CGTCAACTAG ACCAGAGAGT TTGGAGACGC TTTTGCTCTC AAAACTTTCC	1900
AACCACTGTG CCTTCTCACC CACAATCCTG TGTGGAGTTA CTTGCAGGGA	1950
AACCAATGCA AAGGAGACAA ATGCAGTTCA TGGGCTTCTG GACTGATATT	2000
CACCAGGGTC ACAATGTGAT TGGGTTACTT TCTTAACAGT AATCCTAAGT	2050
CTTGCAGCAT TAAAAA AAAA AATCATCACA ATGAAGAAAA AAAAACCCAA	2100
AAAATCTAAA ATCTAAAATT CATCATCATC ATCAACAACA ACAACAACAA	2150
CAACAACAAA ACCACCCACT TCAGGTTGAG TTTATGAAGA GGGCAGAACA	2200
ATTTAGTTGT AATTATAGAG ATGTTTATAT GTATAGTTGT AAATATTCAT	2250
CCATTCTTTT ACAGAGTTGT TGCTCCCCTC ATATAAATTG ACTGAGGAGC	2300
CGCAACCTTT AGCTCCTACC ATCTTCCTCC TACTGTCTGG GAGTTAAAAA	2350
TGTCATCTGA TGTTCTATTG CAGAAACATC ATTAAATATA ACCCAACAGT	2400
AGGAAGTTGA ATATATCAGC CAACAAATTA CTATGATAGT AAGTCCTGTG	2450
TATTCATTCG CATGTTCTT GAAAAAATG AATCCTCTAG CTCTCAGTGG	2500

32/45

FIGURE 12C

AAAGTTTAAA	ACTAGAAACA	TCTGGAGCCC	TAGACAATAT	TTTAGTGTGG	2550
CGGTAGTCTC	CTGGCTTTGG	GCTCCAGGGA	AAATTCACCTC	TTGCCCAAGC	2600
AGATAAGCCC	AGATGACTAG	AAGCAATTTT	CA ¹ TAGGAAG	TGGCAAGAAC	2650
ATTTGAAGAA	GTAAC ¹ TCAT	ATCTATTTAT	CTATATACCT	ATAGTATTTA	2700
TATACTTGTA	GACATATAGA	TGTATAAAAT	GAAAGCCCAT	AGCCAGCCCC	2750
ACTCAGTCAA	CAATTCTCAA	AAGAGCAATA	TGAAGCAGTC	ATTTGGTGGG	2800
GTTTCGTATGC	AAGAAAATAA	AAAAACGTCA	TGAATTCCAT	ATGAATACCA	2850
CGCTAAAGTA	ATGCAAAACA	ATGTGCTGCC	TCAGTGTGTG	TGTGTGTGTG	2900
TGTGTGTGTG	GTGGGTTCGT	GCATGTATGT	GTGCGTGTGT	GTGTGTGTGT	2950
GTGTGTGTGT	GTGTGTGTGC	GTGTGTGTTT	GTTTAGGGGT	TTTTATAAAC	3000
AACTTTTTTT	ATAAAGCACA	CTTTAGTTTA	CAATCTCTCT	TTATAACTGT	3050
TATAAATTTT	TAAACAACCC	AAAATGCGTT	CCATATAAAG	AAATGGCAAG	3100
TTATTTAGCT	ATCAAGATTT	TACATGTTTT	CTTTTAACTT	TTTTGTACAA	3150
TTGCATAGAC	GTGTAAAACC	TGCCATTGTT	AACAAAACAA	TAACAGACTT	3200
AGAAACTACT	GAAATCTACA	GTATAGTACC	ACTACCCTTC	ACAAAAATAT	3250
AGATTTTATT	TCTTGTAAC	TCTTACTGTC	TAATCCTCTT	TGTTGTACGA	3300
ATATTATAAA	AACCATGCGG	GAATCAGGAG	TTGTAAAACA	TTTATTCTGC	3350
TCCTTCTTCA	TCTGTCATGA	CTGAAACTAA	GGACTCCATC	GCTCTGCCCC	3400
AATCATCTGC	CATGTGGAAA	AGGCTTCCTA	CATTGTGTCC	TCTCTCATTG	3450
GCTTTCCGGG	GGCATTTCTT	CCTCTGAAAC	TAGGGAAGGA	GTTGTTGAGT	3500
TGCTCCATCA	CTTCTTCTAA	CCCTGTGCTT	GTGTCCTGGG	GAGGACTCAG	3550
AAGATCTTCC	TCACCCATAG	ATTCTGAAGT	TTGACTGCCA	ACCACTCGGA	3600
GCAGCATAGG	CTGACTGCTA	TCTGACCTCT	GCAGAGAGGT	GGAAGGAGAG	3650
GACACCGTGG	TGCCATTAC	CTTAGCTTCA	GCCTGGGGCT	GCTCCAGGAG	3700
CTGTCTCAGT	CTATGTAAC	GAGACTCCAG	CTGTTTATTG	TGGTCTTCCA	3750

SEQUENCE LISTING

FIGURE 12D

GGATTTGCAT	CCTGGCTTCC	AGGCGTCCTT	TGTGTTGGCG	CAGTAGCTTA	3800
GCCTCAGCAA	TGAGCTCAGC	ATCCCTGGGA	CTCTGAGGAG	AGGTGGGCAT	3850
CATCTCAGGA	GGAGATGGCA	GTGGAGACAG	GCCTTTATGC	TCATGCTGCT	3900
GCTTCAGGCG	ATCATATTCT	GCTTGACAGT	TCCTGTTTTT	TTCTCAAGA	3950
TCTGCTAGGA	TTCTCTCTAG	CTCCCCTCTT	TCCTCACTCT	CTAAGGAAAT	4000
CAAGATCTGG	GCAGGACTAC	GAGGCTGGCT	CAGGGGGGAG	TCCTGGTTCA	4050
AACTTTGGCA	GTAATGCTGG	ATTAACAAAT	GTTTCATCATC	TATGCTCTCA	4100
TTAGGAGAGA	TGCTATCATT	TAGATAAGAT	CCATTGCTGT	TTTCCATTTT	4150
TGCTAGCCTG	CTAGCATAAT	GTTCAATGCG	TGAATGAGTA	TCATCGTGTG	4200
AAAGCTGGGG	GGACGAGGCA	GGCGCAGAAT	CTACTGGCCA	GAAGTTGATC	4250
AGAGTAACGG	GAGTTTCCAT	GTTGTCCCCC	TCTAACACAG	TCTGCACTGG	4300
CAGGTAGCCC	ATTCGGGGAT	GCTTCGCAAA	ATACCTTTTG	GTTTCAAATT	4350
TGTTTTTTAG	TACCTTGGCG	AAGTCGCGAA	CATCTTCTCC	GGATGTAGTC	4400
GGAGTGCAAT	ACTCTACCAT	GGGGTAGTGC	ATTTTATGGC	CCTTTGCAAC	4450
TCGGCCAGAA	AAAAAGCAAC	TTTGGCAGAT	GTCATAATTA	AAATGCTTTA	4500
GGCTTCTGTA	CCTGAATCCA	ATGATTGGAC	ACTCCTTACA	GATGTTACAC	4550
TTGGCTTGAT	GCTTGGCAGT	TTCAGCAGCA	GCCACTCTGT	GCAAGACGGG	4600
CAGCCACACC	ATAGACTGGG	GTTCCAGGCG	CATCCAGTCA	AGGAAGAGAG	4650
CAGCTTCAAT	CTCAGGTTTA	TTATTGGCAA	ATTGGAAGCA	GCTCCTGACA	4700
CTCGGCTCAA	TGTTACTGCC	CCCAAAGGAA	GCAACTTCAC	CCAACTGTCT	4750
TGGGATTTGA	ATAGAATCAT	GCAGAAGAAG	ACCCAGCCTA	CGCTGGTCAC	4800
AAAAGCCAGT	TGAACCTGCC	ACTTGCTTGA	AAAGGTATCT	GTACTTGTCT	4850
TCCAAGTGTG	CTTTACACAG	AGAAATGATG	CCAGTTTTAA	AAGACAGGAC	4900
ACGGATCCTC	CCTGTTTCGT	CCGTATCATA	AACATTGAGA	AGCCAGTTGA	4950
GACACATATC	CACACAGAGA	GGGACATTGA	CCAGATTGTT	GTGCTCTTGC	5000
TCCAGACGAT	CATAAATTGT	AGTCAAACAG	TTAATTATCT	GCAGGATATC	5050

34/45

FIGURE 12E

CATGGGCTGG	TCATTTTGCT	TGAGGTTGTG	CTGGTCCAGG	GCATCACATG	5100
CAGCTGACAG	GCTCAAGAGA	TCCAAGCAAA	GGGCCTTCTG	GAGCCTTCTG	5150
AGCTTCATGG	CAGTCCTATA	CGCGGAGAAC	CTGACATTAT	TCAGGTCAGC	5200
TAAAGACTGG	TAGAGCTCTG	TCATTTTGGG	GTGGTCCCAA	CAAGTGGTTT	5250
GGGTCTCGTG	GTTGATATAG	TAGGGCACTT	TGTTTGGTGA	GATGGCTCTC	5300
TCCCAGGGAC	CCTGAACTGA	AGTGGAAGG	AAGTGCTGGG	ATGCAGGACC	5350
AAAGTCCCTG	TGGGCTTCAT	GCAGCTGTCT	GACACGGTCC	TCCACAGCCA	5400
CCTGTAGAAG	CCTCCATCTG	GTATTGAGAT	CTTCCAAAGT	GCTGAGGTTA	5450
TAAGGTGAGA	GCTGAATGCC	CAGTGTGGTC	AGCTGATGTG	CAAGGTCATT	5500
GACACGATTG	ACATTCTCTT	TAAGAGGTGC	AATTTCTCCC	CGAAGTGCCT	5550
TGACTTTTTC	AAGGTGATCT	TGCAGAGAGT	CAATGAGGAG	ATCCCCCACT	5600
GGCTGCCAGG	ATCCCTTGAT	CACCTCAGCT	TGGCGCAACT	TGAGGTCCAG	5650
TTCATCGGCA	GCTTCCTGAA	GTTCTGGAG	TCTTTCAAGA	GCTTCATCTA	5700
TTTTTCTCTG	CCAATCAGCT	GAGCGCAGGT	TCAATTTGTC	CCATTGAGCG	5750
TTGACCTCTT	CAGCCTGCTT	TCGTAGGAGC	CGAGTGACAT	TCTGAGCTCT	5800
TTCTTCAGGA	GGCAGTTCTC	TGGGCTCCTG	GTAGAGTTTC	TCTAGTCCCT	5850
CCAAAGGCTG	CTCTGTCAGA	AATATTCTCA	CAGTCTCCAG	AGTACTCATG	5900
ATTACAGGTT	CTTTAGTTTT	CAATTCCCTC	TTGAAGGCC	TATGTATATC	5950
ATTCTGCTTC	TGAACTGCTG	GGAAATCACC	ACCGATGGGT	GCCTGACGGC	6000
TCAGTTCATC	ATCTTTCAGC	TGTAGCCAAA	CAAGAAGTTC	CTGAAGAGAA	6050
AGATGCAAAC	GCTTCCACTG	GTCAGAACTT	GCTTCCAAAT	GGGACCTAAT	6100
GTTGAGAGAC	TTTTTCTGAA	GTTCACTCCA	CTTGAAATTC	ATGTTATCCA	6150
AACGTCTTTG	TAACAGGGGT	GCTTCATCCG	AACCTTCCAG	GGATCTCAGG	6200
ATTTTTTGGC	CATTTTCATC	AAGATTGTGA	TAGATATCTG	TGTGAGTTTC	6250
AATTTCTCCT	TGGAGATCTT	GCCATGGTTT	CATCAGCTCT	CTGACTCCCC	6300
TGGAGTCTTC	TAGGAGCTTC	TCCTTACGGG	AAGCGTCCTG	TAGGACATTG	6350

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FIGURE 12F

GCAGTTGTTT CTGCTTCCGT AATCCAGGAA AGAAACTTCT CCAGGTCCAG	6400
AGGGAAGTGC TGCAGTAATC TATGAGTTTC TTCAAAGCA GCCTCTTGCT	6450
CACTTACTCT TTTATGAATG TTTCCCCAAG AAGTATTGAT ATTCTCTGTT	6500
ATCATGTGTA CTTTCTGGT ATCATCAGCA GAATAGTCCC GAAGAAGTTT	6550
CAGTGCCAAA TCATTTGCCA CGTCTACACT TATCTGCCGT TGACGGAGGT	6600
CTTTGGCCAA CTGCTTGGTT TCTGTGATCT TCTTTTGGAT TGCATCTACT	6650
GTGTGAGGAC CTTCTTTCCA TGAGTCAAGC TTGCCTCTGA CCTGTCTAT	6700
GACCTGTTTC GCTTCTTCCT TAGCTTCCAG CCATTGTGTT GAATCCTTTA	6750
ACATTTCAAT CAACTGTTGT CTCCTGTTCT GCAGCTGTTT TTGAACCTCA	6800
TCCCACTGAA TCTGAATTCT TTCAATTCGA TCAGTAATGA TTGTTCTAGC	6850
TTCTTGATTG CTGGTTTTGT TTTTCAAATT CTGGGCAGCA GTAATGAGTT	6900
CTTCCAATTG GGGGCGTCTC TGTTCCAAAT CTGCAAGTGT TGCCTTCTGT	6950
TTGATGATCA TTTCATTGAT GTCTTCCAGA TCACCCACCA TCACTCTCTG	7000
TGATTTTATA ACTCGATCAA GCAGAGACAG CCAGTCTGTA AGTTCTGTCC	7050
AAGCTCGGTT GAAGTCTGCC AGTGCAGGTA CCTCCAACAG CAAAGAAGAT	7100
GGCATTTCTA GTTTGGAGAT GACAGTTTCC TTAGTAACCA CAGATTGTGT	7150
CACTAGAGTA ACAGTCTGAC TGGCAGAGGC TCCAGTAGTG CTCAGTCCAG	7200
GGGCACGGTC AGGCTGCTTT GTCCTCAGCT CCCGAAGTAA ATGGTTTACA	7250
GCCTCCCACT CAGACCTCAG ATCTTCTAAC TTCCTCTTCA CTGGCTGAGT	7300
GCTTGGTTTT TCCTTATACA AATGCTGCCC TTTGACAAA AGCCTTTCCA	7350
CATCCGCTTG TTTACCGTGA ACTGTTACTT CAATCTCCTT TATGTCAAAC	7400
GGTCTGCCT GACTTGGTTG GTTATAAATT TCCAAGTGGT TTCTAATAGG	7450
AGAGACCCAC AGAAGCAGGT GATCCAGCTG CTCTTCAAGC TGCCTAAAAT	7500
CTTTTAAGTG AACCTCAAGC TCTCCTTGTT TCTCAGGTAA AGCTCTGGAG	7550
ACCTTTATCC ACTGGAGATT TGTCTGTTTG AGCTTCTTTT CAAGTTTATC	7600

36/45

FIGURE 12G

TTGCTCTTCT	GGCCTTATGG	GAGCACTTAC	AAGTACTGCT	CCTCCTGTTT	7650
CATTTAATTG	TTTtagaatt	CCCTGGCGCA	GGGGCAACTC	TTCTGCCAGT	7700
AACTTGACTT	GTTCAAGTTG	TTCTTTTAGC	TGCTGCTCAT	CTCCAAGTGG	7750
AGTAATAGCA	ATGTTATCTG	CTTCTTCCAG	CCACAAAACA	AATTCATTTA	7800
AATCTCTTTG	AAATTCTGAC	AAGACATTCT	TTTGTCTTTC	AATCCTCTTT	7850
CTCCTTTCTG	CCAGCTCTTT	GCAGATGTCG	TGCCACCGCA	GACTCAAGCT	7900
TCCTAATTTT	TCTTGTAGAA	TATTGACATC	TGTTTTTGAA	GACTGTTGAA	7950
TTATTTCTTC	CCCAGTTGCA	TTCAGTGTTT	TGACAACAGC	TTGACGCTGC	8000
CCAATGCCAT	CCTGGAGTTC	CTTAAGATAC	CATTTGTATT	TAGCATGTTT	8050
CCAGTTTTCA	GGATTTTGTT	TCTTTTGAA	AAACTGTTCA	ACTTCATTCA	8100
GCCATTGATT	AAATACCTTC	ATATCATAAT	GAAAGTGTCG	CCATTTTTCA	8150
ACTGATCTGT	CGAATCGCCC	TTGTCGTTCC	TTGTACATTC	TATGAAGTTT	8200
TTCCCCCTGG	AAATCCATCT	GTGCCACGGC	TTCTGTACT	TTCACCTTTT	8250
CCATGGAGGT	GGCACTTTGC	AAGGCTGCTG	TCTTCTTCTT	GTGAATAATA	8300
TCAATCCGAC	CTGAGATTTG	TTGCAAATTG	TCTTTTATAT	TCTTAAGAGA	8350
CTCCTCTTGC	TTAAAAAGAT	CTTCAAAATC	TTAGCACAG	AGTTCAGGAG	8400
TATTTAGAAG	ATGATCAACT	TCTGAAAGAG	CTTGTAAGAT	ATGACTGATC	8450
TCGGTCAAAT	AAGTAGAAGG	CACATAAGAA	ACATCCAAAG	GCATATCTTC	8500
AGTCGTCACT	ACCATAGTTT	CTTCATGGAG	AGTGTGAATT	TGTGCAAAGT	8550
TGAGTCTTCG	AAACTGAGCA	AAATTGCTCT	CAATTTGCCG	CCAGCGCTTG	8600
CTGAGCTGGA	TCTGAGTTGG	CTCCACTGCC	ATTGCGGCCC	CATTCTCAGA	8650
CAAGCCCTCA	GCTTGCCTGC	GCACTGCATT	CAGCTCCTCT	TTCTTCTTCT	8700
GCAATTCACG	ATCAATTTCC	TTTAATTTTC	TTTCATCTCT	GGGTTCCAGT	8750
AGGCTGGCTA	ATTTTTTTTC	AATTTTCATCC	AAGCATTTCA	GGAGATCATC	8800
AGCCTGCCTC	TTGTACTGAT	ACCACTGGTG	AGAAATTTCT	AGGGCCTTTT	8850

CONTINUITY SHEET (RULE 28)

37/45

FIGURE 12H

TTCTTCTTTG	AGACCTCAAA	TCCTTGAGAG	CATTATGTTT	TGTCTGTAAC	8900
AGCTGCTGTT	TTATCTTTAT	TTCCTCTCGC	TTTCTCTCAT	CTGTGATTCT	8950
TTGTTGTAAG	TTGTCTCCTC	TTTGCAACAA	TTCATTTACA	GTACCCTCAT	9000
TGTCTTCACT	CATATCTTTA	TTGAAGTCTT	CCTCTTTCAG	ATTACCCCCC	9050
TGCTGAATTT	CAGCCTCCAG	TGGTTCAAGC	AATTTTTGTA	TATCTGAGTT	9100
AAACTGCTCC	AATTCCTTCA	AAGGAATGGA	GGCCTTTCCA	GTCTTAATTC	9150
TGTGAGAAAT	AGCTGCAAAT	CGACGGTTGA	GCTCAGAGAT	TTGGGGCTCT	9200
ACTACTTTCC	TGCAGTGGTC	ACCGCGGTTT	GCCATCAATT	TTGCTGCTTG	9250
GTCACGTGTG	GAGTCCACCT	TTGGGCGCAT	GTCATTCATT	TCAGCCTTTA	9300
AACGCTTAAG	AATGTCTTCC	TTTTGTTGTG	GTTTCTTCTT	TTCAGACTCA	9350
TCTAAAAGTT	CATCTGCATG	AATGATCCAC	TTTGTGATTT	GTTCTATGTT	9400
CTGATCAAAG	GTTTCCATGT	GTTTCTGGTA	TTCCAACAAA	AGATTTAGCC	9450
ATTCTTCTAC	TCTGGAGGTG	ACAGCTATCC	AGTTACTGTT	CAGAAGACTC	9500
AGTTTATCTT	CTACCAAGGT	TTCTTTCTTG	CCCAACACCA	TTTTCAAAGA	9550
CTCTCCTAAT	TCTGTAACAC	TCTTCAAGTG	AGCCTTCTGT	TTCTCAATCT	9600
CTTTTTGAGT	AGCCTTTCCC	CAGGCAACTT	CAGAATCCAA	ATTACTTGGC	9650
ATTCCTTCAA	CTGCTGATCT	CTTCGTCAAT	TCTGTATCTG	TTGCTGCCAG	9700
CCATTCTGTT	AAGACATTCA	TTTCCTTTCT	CATCTTACGG	GACAACTTCA	9750
AGCATTTCTC	CAACTGTTGC	TTTCTCTCTG	TTACCTTCGC	ACCCAACTCA	9800
TTGTAATGCA	ATTTCAAAGC	TGTTACTCGT	TCATCAAGCT	CTTTGGGATT	9850
TTCTGTCTGC	TTTTTCTGTA	CAATTTGACG	TCCGGTTTTA	ATCACCATTT	9900
CCACTTCAGA	CTTGACTTCA	CTCAGGCTTT	TATACAAGTT	CACACAATGA	9950
CTTAGTTGTG	ACTGAATTAC	TTCTGTTC	ACACTCTTGG	TTTCCAATGC	10000
AGGCAAATGC	ATCTTGACTT	CATCTAAAAT	CATCTTACTT	TCCTCTAGAC	10050
GTTGTTCAAA	ATTGGCTGGT	TTTTGGAATA	ATCGAAATTT	CATGGAGACA	10100
TCTTGTAATT	TTTTCTGTGC	AACATCAATT	TGTGAAAGAA	CCCTTTGGTT	10150

38/45

FIGURE 12I

GGCATCCTTC	CCCTGGTTAT	GTTTCTTCAT	TTCTTCTAAA	CTTATCTCAT	10200
GACTTGTCAA	ATCTGATTGG	ATTTTCTGGG	CTTCCTGAGG	CATTTGAGCT	10250
GCATCCACCT	TGTCAGTGAT	ATAAGCTGCC	AACTGCTTGT	CAATGAATTC	10300
AAGCGACTCC	TGAATTAAGT	GCAAGGACTT	TTCAATTTCC	TGGGCAGACT	10350
GGATACTCTG	TTCAAGCAAC	TTTGTTTTCC	TCACAGCCTC	TTCATGTAGT	10400
TCCCTCCAAC	GAGAATTAAA	CGTCTCAAGC	TCCTCATTGA	TCAGTTCATC	10450
CATGACTCCT	CCATCTGTAA	GAGTCTGTGC	CAATAGACGA	ATCTGATTTG	10500
GGTTCTCCTC	TGAATGATGC	ATCAGATTTT	CAAGAGATTC	TAGCACTTCA	10550
GTGATTTCTC	CAGGTCTGTC	AGGAACATTT	TCCATGGTTT	TAAGTTTCAA	10600
TTCTACTTCA	TTGAGCCACT	TGTTTGCTTT	CTCTAAATAT	GACAATAACT	10650
CATGCCAACA	TGCCCCAACT	TCTTCCAAAG	TTTTGCATTT	TCCATTGAGC	10700
CTGGTGCACA	GCCATTGGTA	GTTGGTGGTC	AGAGTTTCAA	GTTCTCTTTT	10750
TAAGGCCTCT	TGTGCTGAGG	GTGGAGCGTG	AGCTATTACA	CTATTTACAG	10800
TCTCAGTAAG	GAGTTTCACT	TTAGTTTCTT	TTTGTAGTGC	CTCTTCTTTA	10850
GCTCTCTTCA	TTTCTTCAAC	AGCAGTCTGT	AATTCATCTG	GAGTTTATA	10900
TTCAAAATCT	CTCTCTAGAT	ATTCTTCTTC	AGCTTGTGTC	ATCCACTCAT	10950
GCATCTCTGA	TAGATCTTTT	TGGAGGCTTA	CGGTTTTATC	CAAACCTGCC	11000
TTTAAGGCTT	CCTTTCTGGT	GTAGACCTGG	CGGCATATGT	GATCCCACTG	11050
AGTGTTAAGC	TCTCTAAGTT	CTGTCTCCAG	TCTGGATGCA	AACTCAAGTT	11100
CAGCTTCACT	CTTTATCTTC	TGCCCCACCTT	CATTAACT	ATTTAACTG	11150
GGCTGAATTG	TTTGAATATC	ACCAACTAAA	AGTCTGCATT	GTTTGAGCTG	11200
TTTTTTCAGG	ATTTGAGCAT	CCCCCAGGGC	AGGCCATTCC	TCTTTCAGGA	11250
AAACATCAAC	TTGAGCCATC	CATTTCTGTA	AGGTTTTTAT	GTGATTCTGA	11300
AATTTTCGAA	GTTTATTCAT	ATGTTCTTCT	AGCTTTTGGC	AGCTTTCCAC	11350
CAACTGGGAG	GAAAGTTTCT	TCCAGTGCCC	CTCAATCTCT	TCAAATTCTG	11400

SEQUENCE LISTING

FIGURE 12J

ACAGATATTT	CTGGCATATT	TCTGAAGGTG	CTTTCTTGGC	CATCTCCTTC	11450
ACAGTGTCAC	TCAGATAGTT	GAAGCCATTT	TGTTGCTCTT	TCAAAGAACT	11500
TTGCAGAGCC	TGTAATTTCC	CGAGTCTCTC	CTCCATTATT	TCATATTCAG	11550
TAACACTAAG	ATAAGGTACA	GAGAGTTTGC	TTTCTGACTG	CTGGATCCAC	11600
GTCCTGATGC	TACTCATTGT	CTCCTGATAG	CGCATTGGTG	GTAAAGTGTC	11650
AAAAATTGTC	TGTAGCTCTT	TCTCTTTGGC	CCTCACACCA	TCAAAGATGT	11700
GGTTAAATG	ATTAGTAAAG	GCCACAAAGT	CTGCATCCAG	AAACATTGGC	11750
CCCTGTCCCT	TTTCTTTTCA	TTGTAGACTC	TGAATTTTTA	ATTGCTCAAT	11800
TTGAGGCTGA	AGAGCTGACA	ATCTGTTGAC	TTCATCCTTA	CAAATTTTTA	11850
ACTGGCTTTT	AATTGCTGTT	GGCTCTGATA	GGGTGGTAGA	CTGGGTTTTC	11900
AACAAGTTTT	CGGCAGTAGT	TGTCATCTGT	TCCAATTGTT	GTAGCTGATT	11950
ATAAAAGGTA	ATGATGTTGG	TTTGATACTC	TAGCCAGTTA	ACTCTCTCAC	12000
TCAGCAATTG	GCAGAATTCT	GTCCACCGGC	TGTTCAAGTTG	TTCTGAAGCT	12050
TGTCTGATAC	TTTCAGCATT	AACACCCTCA	TTTGCCATCT	GTTCCACCAG	12100
GGCCTGAGCT	GATCTGCTGG	CATCTTGACG	TTTTCTGAAC	TTCTCTGCTT	12150
TTTCTCGTGC	TATGGCATTG	ACTTTTTTCT	GCAAGTCTGA	GATGTTGCCT	12200
TCTTTTCGAT	AGACTGCAAA	TTCAGAACTC	TGTAATACAG	CTTCTGAACG	12250
AGTAATCCAA	CTGTGAAGTT	CAGTTATATC	GACATCCAAC	CTTTTCCTGA	12300
GTTCAGAATC	CACAGTTATC	TGCCTCTTCT	TTTGAGGAGG	TGGTGGTGGA	12350
AGTTCCCTCTT	GGGCATGTTT	TACCATGATT	TGTTCCCTTG	TGGTCACCAT	12400
AGTTACCGTT	TCCATTACAG	TTGTCTGTGT	TAGGGATGGT	TGAGTGGTGG	12450
TGACAGCCTG	TGAAATTTGT	GCTGAACTCT	TTTCAAGTTT	TTGGGTTAAA	12500
TTGTCCCAAC	GTTGTGCAAA	GTTTTCCATC	CAGATTTCCA	TCTTTTGAGT	12550
CACTGACTTA	TTTTTCAGTG	CCGAAAGTAG	ATCTTGATTG	AGTGAACCTA	12600
GTTTTTCCAT	GGTTGGCTTT	TTCTTTTCTA	GATCTATTTT	TAAAGTAGAT	12650

40/45

FIGURE 12K

ATTTTGTGAA	GACTTGACAT	CATTTTCATT	TGATCTTTAA	AGCCACTTGT	12700
CTGAATGTTT	TTCATTGCAT	CTTCTTTTTC	TGAAAGCCAT	GTAATAAAAA	12750
GGCACTGTTT	TTCAGTAAAA	TGCTGCCATT	TTAGAAGAAT	ATCTTGTAAT	12800
ACAATCCAGC	GGTCTTCAGT	CCATCTGCAG	ATATTTGCCC	ATCGATCTCC	12850
CAGTACCTTA	AGTTGTTCTT	CCAAAGCAGC	TGTTGCATGA	TCACCGCTGG	12900
ATTCATCAAC	CACTACTACC	ATGTGAGTGA	GCGAGTTGAC	CCTGACCTGC	12950
TCCTGTTCTA	GATCTTCTTG	AAGCACCTTA	TGTTGTTGTA	CTTGGCATT	13000
TAGATCTTCA	AGATCAGGTC	CAAAGGGCTC	TTCTCCATT	TTCTTAGTTC	13050
TCTCTTCAGT	TTTGTTAAC	CAGTCATCTA	GTTCTTTTAA	TTTCTGATTC	13100
TGGAGATCCA	TTAGAATTTT	GTGTAATTTG	CTTTGTTTTT	CCATGCTAGC	13150
TACCCTGAGA	CATTCCCATC	TTGAATTTAG	GAGATTCATT	TGTTCTTGCA	13200
CTTCAGCTTC	TTCATCTTCT	GATAATTTCC	CTTTTCCAAC	TAGTTGACTT	13250
CCTAACTGTA	GAACATTACC	AACAAGTCCT	TGATGAGATG	TCAGATCCAT	13300
CATGAATCCC	TCATGAGCAT	GAAACTGTTT	TTTCACTTCT	TCAACATCAT	13350
TTGAAATCTC	TCCTTGCTCT	CGCAATGTAT	CCTCGGCAGA	AAGAAGCCAT	13400
GAAAGTACTT	CTTCTAAAGC	AGTTTGGTAA	CTATCCAGAT	TTACTTCCGT	13450
CTCCATCAAT	GAAGTGTCAA	GTGACTTGTC	TCTGGGAGCT	TCCAAATGCT	13500
GTGAAGGATA	GGGGCTCTGT	GTGGAATCAG	AGGTGGCAAC	ATAAGCAGCC	13550
TGTGTGAAGG	CATAACTCTT	GAATCGAGGC	TTAGGAGATG	AAGAAGTTTG	13600
TTCATAGCCC	TGTGCTAGAC	TGACTGTGAT	CTGTTGAGAG	TAATGCATCT	13650
GGTGATGTAA	TTGAAAATGT	TCTTCTCTAG	TTACTTTTGA	AGATGTCCTG	13700
GGCAACATTT	CCACTTCTTG	AATGGCTTCA	ATGCTCACTT	GTTGTGGCAA	13750
AACTTGAAAG	AGTGATGTGA	TGTACATTAA	GATGGACTTC	TTGTCTGGAT	13800
AAGTGGTAGC	AACATCTTCA	GGATCAAGAA	GTTTTTCTAT	GCCTAACTGG	13850
CATTTTGCAA	TGTTGAAGGC	ATGTTCCAGT	CTTTGGGTGG	CTGAGTGCTG	13900

SEQUENCE LISTING / PAGE 2

41/45

FIGURE 12L

TGAAACCACA	CTATTCCAAT	CAAACAGGTC	GGGCCTGTGA	CTATGGATAA	13950
GAGCATTCAA	AGCCAACCCG	TCGGACCAGC	TAGAGGTGAA	GTTGATGACG	14000
TTAACCTGTG	GATAATTACG	TGTTGACTGT	CGAACCCAGC	TCAGAAGAAT	14050
CTTTTCACTG	TTGGTTTGCT	GCAATCCAGC	C TGATAGTT	TTCATCACAT	14100
TTTTGACCTG	CCAGTGGAGG	ATTATATTCC	AAATCAAACC	AAGAGTGAGT	14150
TTATGATTTT	CATCCACTAT	GTCAGTGCTT	CCTATATTCA	CTAAATCAAC	14200
ATTATTTTTT	TGTAAGACCC	GCAGTGCCTT	GTTGACATTG	TTCAGGGCAT	14250
GAACCTCTGT	AGATCCCTTT	TCTTTTGGCA	GTTTTTGCCC	TGTAAGGCCT	14300
TCCAAGAGGT	CTAGGAGGCG	TTTTCCATCC	TGCAGGTCAC	TGAAGAGGTT	14350
GTCTATGTGT	TGCTTTCCAA	ACTTAGAAAA	TTGTGCATTT	ATCCATTTTG	14400
TGAATGTTTT	CTTTTGAACA	TCTTCTCTTT	CATAACAGTC	CTCTACTTCT	14450
TCCCACCAAA	GCATTTGGAA	GAAAAAGTAT	ATATCAAGGC	AGGGATAAAA	14500
ATCTTGGTAA	AAGTTTCTCC	CAGTTTTATT	GCTCCAGGAG	GCTTAGGTAC	14550
GATGAGAAGC	CAATAAACTT	CAGCAGCCTT	GACAAAAAAA	AAAAAAAAAA	14600
TAGCACTTCA	AGTCTTCCTA	TTCGTTTTTT	CTATAAAGCT	ATTGCCTTCA	14650
AGAGCGGAAT	TCCTGCAGCC	CGGGGGATCC	ACTAGTTCTA	GAGCGGCCGC	14700
GGGTACAATT	CCGCAGCTTT	TAGAGCAGAA	GTAACACTTC	CGTACAGGCC	14750
TAGAAGTAAA	GGCAACATCC	ACTGAGGAGC	AGTTCTTTGA	TTTGACCCAC	14800
CACCGGATCC	GGGACCTGAA	ATAAAAGACA	AAAAGACTAA	ACTTACCAGT	14850
TAACTTTCTG	GTTTTTTCAGT	TCCTCGAGTA	CCGGATCCTC	TAGAGTCCGG	14900
AGGCTGGATC	GGTCCCGGTG	TCTTCTATGG	AGGTCAAAAC	AGCGTGGATG	14950
GCGTCTCCAG	GCGATCTGAC	GGTTCACTAA	ACGAGCTCTG	CTTATATAGA	15000
CCTCCCACCG	TACACGCCTA	CCGCCCATTG	GCGTCAATGG	GGCGGAGTTG	15050
TTACGACATT	TTGGAAAGTC	CCGTTGATTT	TGGTGCCAAA	ACAAACTCCC	15100
ATTGACGTCA	ATGGGGTGGA	GACTTGAAAA	TCCCCGTGAG	TCAAACCGCT	15150
ATCCACGCCC	ATTGATGTAC	TGCCAAAACC	GCATCACCAT	GGTAATAGCG	15200

42/45

FIGURE 12M

ATGACTAATA	CGTAGATGTA	CTGCCAAGTA	GGAAAGTCCC	ATAAGGTCAT	15250
GTACTGGGCA	TAATGCCAGG	CGGGCCATTT	ACCGTCATTG	ACGTCAATAG	15300
GGGGCGTACT	TGGCATATGA	TACACTTGAT	GTACTGCCAA	GTGGGCAGTT	15350
TACCGTAAAT	ACTCCACCCA	TTGACGTCAA	TGGAAAGTCC	CTATTGGCGT	15400
TACTATGGGA	ACATACGTCA	TTATTGACGT	CAATGGGCGG	GGGTCGTTGG	15450
GCGGTCAGCC	AGGCGGGCCA	TTTACCGTAA	GTTATGTAAC	GACCTGCAGG	15500
TCGACTCTAG	AGGATCTCCC	TAGACAAATA	TTACGCGCTA	TGAGTAACAC	15550
AAAATTATTC	AGATTTCACT	TCCTCTTATT	CAGTTTTCCT	GCGAAAATGG	15600
CCAAATCTTA	CTCGGTTACG	CCCAAATTTA	CTACAACATC	CGCCTAAAAC	15650
CGCGCGAAAA	TTGTCACTTC	CTGTGTACAC	CGGCGCACAC	CAAAAACGTC	15700
ACTTTTGCCA	CATCCGTCGC	TTACATGTGT	TCCGCCACAC	TTGCAACATC	15750
ACACTTCCGC	CACACTACTA	CGTCACCCGC	CCCGTTCCCA	CGCCCCGCGC	15800
CACGTCACAA	ACTCCACCCC	CTCATTATCA	TATTGGCTTC	AATCCAAAAT	15850
AAGGTATATT	ATTGATGATG	CTAGCGGGGC	CCTATATATG	GATCCAATTG	15900
CAATGATCAT	CATGACAGAT	CTGCGCGCGA	TCGATATCAG	CGCTTTAAAT	15950
TTGCGCATGC	TAGCTATAGT	TCTAGAGGTA	CCGGTTGTTA	ACGTTAGCCG	16000
GCTACGTATA	CTCCGGAATA	TTAATAGGCC	TAGGATGCAT	ATGGCGGCCG	16050
GCCGCCTGCA	GCTGGCGCCA	TCGATACGCG	TACGTCGCGA	CCGCGGACAT	16100
GTACAGAGCT	CGAGAAGTAC	TAGTGGCCAC	GTGGGCCGTG	CACCTTAAGC	16150
TTGGCACTGG	CCGTCGTTTT	ACAACGTCGT	GACTGGGAAA	ACCCTGGCGT	16200
TACCCAACTT	AATCGCCTTG	CAGCACATCC	CCCTTTCGCC	AGCTGGCGTA	16250
ATAGCGAAGA	GGCCCGCACC	GATCGCCCTT	CCCAACAGTT	GCGCAGCCTG	16300
AATGGCGAAT	GGCGCCTGAT	GCGGTATTTT	CTCCTTACGC	ATCTGTGCGG	16350
TATTTACAC	CGCATACGTC	AAAGCAACCA	TAGTACGCGC	CCTGTAGCGG	16400
CGCATTAAGC	GCGGCGGGTG	TGGTGGTTAC	GCGCAGCGTG	ACCGCTACAC	16450

SEQUENCE SHEET (RILE 28)

FIGURE 12N

TTGCCAGCGC	CCTAGCGCCC	GCTCCTTTCG	CTTCTTCCC	TTCCTTCTC	16500
GCCACGTTCG	CCGGCTTTCC	CCGTCAAGCT	CTAAATCGGG	GGCTCCCTTT	16550
AGGGTTCGGA	TTTAGTGCTT	TACGGCACCT	CGACCCCAAA	AAACTTGATT	16600
TGGGTGATGG	TTCACGTAGT	GGGCCATCGC	CCTGATAGAC	GGTTTTTCGC	16650
CCTTTGACGT	TGGAGTCCAC	GTTCTTTAAT	AGTGGACTCT	TGTTCCAAAC	16700
TGGAACAACA	CTCAACCCTA	TCTCGGGCTA	TTCTTTTGAT	TTATAAGGGA	16750
TTTTGCCGAT	TTCGGCCTAT	TGGTTAAAAA	ATGAGCTGAT	TTAACAAAAA	16800
TTTAACGCGA	ATTTTAACAA	AATATTAACG	TTTACAATTT	TATGGTGAC	16850
TCTCAGTACA	ATCTGCTCTG	ATGCCGCATA	GTTAAGCCAG	CCCCGACACC	16900
CGCCAACACC	CGCTGACGCG	CCCTGACGGG	CTTGTCTGCT	CCCGGCATCC	16950
GCTTACAGAC	AAGCTGTGAC	CGTCTCCGGG	AGCTGCATGT	GTCAGAGGTT	17000
TTCACCGTCA	TCACCGAAAC	GCGCGAGACG	AAAGGGCCTC	GTGATACGCC	17050
TATTTTATA	GGTTAATGTC	ATGATAATAA	TGGTTTCTTA	GACGTCAGGT	17100
GGCACTTTTC	GGGGAATGT	GCGCGGAACC	CCTATTTGTT	TATTTTCTA	17150
AATACATTCA	AATATGTATC	CGCTCATGAG	ACAATAACCC	TGATAAATGC	17200
TTCAATAATA	TTGAAAAAGG	AAGAGTATGA	GTATTCAACA	TTCCGTGTC	17250
GCCCTTATTC	CCTTTTTTGC	GGCATTTCG	CTTCTGTTT	TTGCTCACCC	17300
AGAAACGCTG	GTGAAAGTAA	AAGATGCTGA	AGATCAGTTG	GGTGACGAG	17350
TGGGTACAT	CGAACTGGAT	CTCAACAGCG	GTAAGATCCT	TGAGAGTTTT	17400
CGCCCCGAAG	AACGTTTTCC	AATGATGAGC	ACTTTTAAAG	TTCTGCTATG	17450
TGGCGCGGTA	TTATCCCGTA	TTGACGCCGG	GCAAGAGCAA	CTCGGTCGCC	17500
GCATACACTA	TTCTCAGAAT	GACTTGGTG	AGTACTCACC	AGTCACAGAA	17550
AAGCATCTTA	CGGATGGCAT	GACAGTAAGA	GAATTATGCA	GTGCTGCCAT	17600
AACCATGAGT	GATAACACTG	CGGCCAACTT	ACTTCTGACA	ACGATCGGAG	17650
GACCGAAGGA	GCTAACCGCT	TTTTTGCACA	ACATGGGGGA	TCATGTAAC	17700

44/45

FIGURE 120

CGCCTTGATC	GTTGGGAACC	GGAGCTGAAT	GAAGCCATAC	CAAACGACGA	17750
GCGTGACACC	ACGATGCCTG	TAGCAATGGC	AACAACGTTG	CGCAAACCTAT	17800
TAACTGGCGA	ACTACTTACT	CTAGCTTCCC	GGCAACAATT	AATAGACTGG	17850
ATGGAGGCGG	ATAAAGTTGC	AGGACCACTT	CTGCGCTCGG	CCCTTCCGGC	17900
TGGCTGGTTT	ATTGCTGATA	AATCTGGAGC	CGGTGAGCGT	GGGTCTCGCG	17950
GTATCATTGC	AGCACTGGGG	CCAGATGGTA	AGCCCTCCCG	TATCGTAGTT	18000
ATCTACACGA	CGGGGAGTCA	GGCAACTATG	GATGAACGAA	ATAGACAGAT	18050
CGCTGAGATA	GGTGCCTCAC	TGATTAAGCA	TTGGTAACTG	TCAGACCAAG	18100
TTTACTCATA	TATACTTTAG	ATTGATTAA	AACTTCATTT	TTAATTTAAA	18150
AGGATCTAGG	TGAAGATCCT	TTTTGATAAT	CTCATGACCA	AAATCCCTTA	18200
ACGTGAGTTT	TCGTTCCACT	GAGCGTCAGA	CCCCGTAGAA	AAGATCAAAG	18250
GATCTTCTTG	AGATCCTTTT	TTTCTGCGCG	TAATCTGCTG	CTTGCAAACA	18300
AAAAAACCAC	CGCTACCAGC	GGTGGTTTGT	TTGCCGGATC	AAGAGCTACC	18350
AACTCTTTTT	CCGAAGGTAA	CTGGCTTCAG	CAGAGCGCAG	ATACCAAATA	18400
CTGTTCTTCT	AGTGTAGCCG	TAGTTAGGCC	ACCACTTCAA	GAACTCTGTA	18450
GCACCCCTTA	CATACCTCGC	TCTGCTAATC	CTGTTACCAG	TGGCTGCTGC	18500
CAGTGGCGAT	AAGTCGTGTC	TTACCGGGTT	GGA CTCAAGA	CGATAGTTAC	18550
CGGATAAGGC	GCAGCGGTCG	GGCTGAACGG	GGGGTTCGTG	CACACAGCCC	18600
AGCTTGGAGC	GAACGACCTA	CACCGAACTG	AGATACCTAC	AGCGTGAGCT	18650
ATGAGAAAGC	GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	AGGTATCCGG	18700
TAAGCGGCAG	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	TCCAGGGGGA	18750
AACGCTGGT	ATCTTTATAG	TCCTGTCGGG	TTTCGCCACC	TCTGACTTGA	18800
GCGTCGATTT	TTGTGATGCT	CGTCAGGGGG	GCGGAGCCTA	TGGAAAAACG	18850
CCAGCAACGC	GGCCTTTTTA	CGGTTCTGG	CCTTTTGCTG	GCCTTTTGCT	18900
CACATGTTCT	TTCCTGCGTT	ATCCCCTGAT	TCTGTGGATA	ACCGTATTAC	18950

SEQUENCE LIST (PAGE 98)

45/45

FIGURE 12P

CGCCTTTGAG	TGAGCTGATA	CCGCTCGCCG	CAGCCGAACG	ACCGAGCGCA	19000
GCGAGTCAGT	GAGCGAGGAA	GCGGAAGAGC	GCCCAATACG	CAAACCGCCT	19050
CTCCCCGCGC	GTTGGCCGAT	TCATTAATGC	AGCTGGCACG	ACAGGTTTCC	19100
CGACTGGAAA	GCGGGCAGTG	AGCGCAACGC	AATTAATGTG	AGTTAGCTCA	19150
CTCATTAGGC	ACCCCAGGCT	TTACACTTTA	TGCTTCCGGC	TCGTATGTTG	19200
TGTGGAATTG	TGAGCGGATA	ACAATTTTAC	ACAGGAAACA	GCTATGACCA	19250
TGATTACGAA	TTCGAATGGC	CATGGGACGT	CGACCTGAGG	TAATTATAAC	19300
CCGGGCC					19307

